

PR	23-APR-1999;	99US-0130899;
PR	28-APR-1999;	99US-0133449;
PR	30-APR-1999;	99US-0132048;
PR	30-APR-1999;	99US-0132407;
PR	04-MAY-1999;	99US-0132484;
PR	05-MAY-1999;	99US-0132485;
PR	06-MAY-1999;	99US-0132486;
PR	06-MAY-1999;	99US-0132487;
PR	07-MAY-1999;	99US-0132863;
PR	11-MAY-1999;	99US-0134256;
PR	14-MAY-1999;	99US-0134218;
PR	14-MAY-1999;	99US-0134219;
PR	14-MAY-1999;	99US-0134221;
PR	14-MAY-1999;	99US-0134370;
PR	18-MAY-1999;	99US-0134768;
PR	19-MAY-1999;	99US-0134941;
PR	20-MAY-1999;	99US-0135124;
PR	21-MAY-1999;	99US-0135353;
PR	24-MAY-1999;	99US-0135629;
PR	25-MAY-1999;	99US-0136022;
PR	27-MAY-1999;	99US-0136392;
PR	28-MAY-1999;	99US-0136782;
PR	01-JUN-1999;	99US-0137222;
PR	03-JUN-1999;	99US-0137528;
PR	04-JUN-1999;	99US-0137502;
PR	07-JUN-1999;	99US-0137724;
PR	08-JUN-1999;	99US-0138094;
PR	10-JUN-1999;	99US-0138540;
PR	10-JUN-1999;	99US-0138847;
PR	14-JUN-1999;	99US-0139119;
PR	16-JUN-1999;	99US-0139452;
PR	16-JUN-1999;	99US-0139453;
PR	17-JUN-1999;	99US-0139492;
PR	18-JUN-1999;	99US-0139454;
PR	18-JUN-1999;	99US-0139455;
PR	18-JUN-1999;	99US-0139456;
PR	18-JUN-1999;	99US-0139461;
PR	18-JUN-1999;	99US-0139462;
PR	18-JUN-1999;	99US-0139463;
PR	18-JUN-1999;	99US-0139750;
PR	18-JUN-1999;	99US-0139458;
PR	18-JUN-1999;	99US-0139459;
PR	18-JUN-1999;	99US-0139459;
PR	18-JUN-1999;	99US-0139460;
PR	21-JUN-1999;	99US-0139817;
PR	22-JUN-1999;	99US-0139899;
PR	23-JUN-1999;	99US-0140353;
PR	23-JUN-1999;	99US-0140354;
PR	24-JUN-1999;	99US-0140695;
PR	28-JUN-1999;	99US-0140823;
PR	30-JUN-1999;	99US-0140991;
PR	30-JUN-1999;	99US-0141287;
PR	01-JUL-1999;	99US-0141842;
PR	01-JUL-1999;	99US-0142154;
PR	02-JUL-1999;	99US-0142055;
PR	06-JUL-1999;	99US-0142390;
PR	08-JUL-1999;	99US-0142803;
PR	09-JUL-1999;	99US-0142920;
PR	12-JUL-1999;	99US-0142977;
PR	13-JUL-1999;	99US-0143542;
PR	14-JUL-1999;	99US-0143624;
PR	15-JUL-1999;	99US-0144005;
PR	16-JUL-1999;	99US-0144085;
PR	16-JUL-1999;	99US-0144086;
PR	19-JUL-1999;	99US-0144325;
PR	19-JUL-1999;	99US-0144331;
PR	19-JUL-1999;	99US-0144332;
PR	19-JUL-1999;	99US-0144333;
PR	19-JUL-1999;	99US-0144334;
PR	19-JUL-1999;	99US-0144335;
PR	20-JUL-1999;	99US-0144352;
PR	20-JUL-1999;	99US-0144632;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 10:31:21 ; Search time 108 Seconds

(without alignments)
1182.741 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRPSPNTVLPIQTP.....KNLNFNIADAFGVGDKSDD 495

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:.*
1: sp_archea:.*
2: sp_bacteria:.*
3: sp_fungi:.*
4: sp_human:.*
5: sp_invertebrate:.*
6: sp_mammal:.*
7: sp_mhc:.*
8: sp_organelle:.*
9: sp_phage:.*
10: sp_plant:.*
11: sp_rodent:.*
12: sp_virus:.*
13: sp_vertibrate:.*
14: sp_unclassified:.*
15: sp_virus:.*
16: sp_bacteriap:.*
17: sp_archeap:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2593	100.0	495	10 Q39016	Q39016 arabidopsis
2	2577	99.4	495	10 Q949P0	Q949P0 arabidopsis
3	2536	97.8	557	10 Q9LQH7	Q9LQH7 arabidopsis
4	2458	94.8	501	10 Q38869	Q38869 arabidopsis
5	2030	78.3	490	10 Q24430	Q24430 glycine max
6	1969.5	76.0	496	10 Q93X19	Q93X19 solanum tub
7	1844.5	71.1	490	10 Q42396	Q42396 arabidopsis
8	1773	68.4	551	10 Q9FXQ3	Q9FXQ3 oryza sativ
9	1752	67.6	492	10 Q04417	Q04417 zea mays (m
10	1751	67.5	487	10 Q43676	Q43676 phaseolus m
11	1746	67.3	558	10 Q8LVP8	Q8LVP8 cucurbita m
12	1745	67.3	554	10 Q04123	Q04123 zea mays (m
13	1742	67.2	556	10 Q38871	Q38871 arabidopsis
14	1739.5	67.1	578	10 Q93XJ0	Q93XJ0 solanum tub
15	1738	67.0	571	10 Q8LPV9	Q8LPV9 cucurbita m
16	1733.5	66.9	578	10 Q93VF3	Q93VF3 nicotiana t

17	1731	66.8	544	10 Q38872	Q38872 arabidopsis
18	1728	66.6	581	10 Q93YF4	Q93YF4 nicotiana t
19	1719	66.3	646	10 Q38870	Q38870 arabidopsis
20	1717.5	66.2	578	10 Q24460	Q24460 tortula tur
21	1709.5	65.9	573	10 P93838	P93838 cucurbita p
22	1709	65.9	483	10 Q39014	Q39014 arabidopsis
23	1708	65.9	581	10 Q93YF7	Q93YF7 nicotiana b
24	1700.5	65.6	484	10 Q9SZM3	Q9SZM3 arabidopsis
25	1672.5	64.5	639	10 Q82107	Q82107 zea mays (m
26	1671	64.4	565	10 Q8H544	Q8H544 oryza sativ
27	1640.5	63.3	583	10 Q9ZV15	Q9ZV15 arabidopsis
28	1630	62.9	451	10 Q41789	Q41789 zea mays (m
29	1592	61.4	542	10 Q9SNK9	Q9SNK9 oryza sativ
30	1592	61.4	542	10 Q8GV21	Q8GV21 oryza sativ
31	1592	61.4	570	10 Q8H889	Q8H889 oryza sativ
32	1587	61.2	542	10 Q65003	Q65003 oryza sativ
33	1583	61.0	542	10 Q8H9A7	Q8H9A7 oryza sativ
34	1531.5	59.1	548	10 Q9S724	Q9S724 marchantia
35	1524.5	58.8	548	10 Q9S786	Q9S786 marchantia
36	1509.5	58.2	528	10 Q8VYE7	Q8VYE7 arabidopsis
37	1506.5	58.1	528	10 Q9FMP5	Q9FMP5 arabidopsis
38	1484.5	57.3	540	10 Q81390	Q81390 nicotiana t
39	1484	57.2	533	10 Q8GTY8	Q8GTY8 oryza sativ
40	1482	57.2	531	10 Q94900	Q94900 arabidopsis
41	1482	57.2	531	10 Q9ZSA2	Q9ZSA2 arabidopsis
42	1480	57.1	518	10 Q9AXA7	Q9AXA7 oryza sativ
43	1480	57.1	531	10 Q41790	Q41790 zea mays (m
44	1475	56.9	347	10 Q94IQ5	Q94IQ5 psophocarpu
45	1473	56.8	553	10 Q8RW36	Q8RW36 lycopersico

ALIGNMENTS

RESULT 1
Q39016 PRELIMINARY; PRT; 495 AA.
ID Q39016
AC Q39016;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Calcium-dependent protein kinase.
GN AtCDPK2.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=94359455; PubMed=8078458;
RA Urao T., Katagiri T., Mizoguchi T., Yamaguchi-Shinozaki K.,
RA Hayashida N., Shinozaki K.;
RT "Two genes that encode Ca2+-dependent protein kinases are induced by
RT drought and high-salt stresses in Arabidopsis thaliana.";
RL Mol. Genet. 244:331-340(1994).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; D21806; BAA04830.1; -;
DR HSSP; P02593; 1FW4.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR007119; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR Pfam; PF00036; ehand; 4;
DR ProDom; PD0000012; EF-hand; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFH; 4.
DR SMART; SM00020; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE F1504.8.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RN [2]
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN [3]
RP SEQUENCE FROM N.A.
RA Ecker J.R.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN [3]
RP SEQUENCE FROM N.A.
RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao O., Johnson-Hopson C.,
RA Khan S., Kim C., Altrati H., Bei B., Chin C., Chiou J., Choi E.,
RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Pederspiel N.,
RA Theologis A., Ecker J.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AC007887; AA79386.1; -;
DR HSSP; P02593; 1FW4.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00054; EFH; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 557 AA; 63397 MW; 7E92BA5A6B3A240B CRC64;

Query Match 97.8%; Score 2536; DB 10; Length 557;
Best Local Similarity 88.5%; Pred. No. 1.Se-182;
Matches 493; Conservative 0; Mismatches 2; Indels 62; Gaps 1;

QY 1 METKPNRPSNTVLPYQTPRLRDHYLLGKLGQGGFTTYLCTEKSTANYACKSIPKR 60
DB 1 METKPNRPSNTVLPYQTPRLRDHYLLGKLGQGGFTTYLCTEKSTANYACKSIPKR 60
QY 61 KLVCREDEYDVWREIQIMHLSHPNVVRKGYEDSVFVHIVMEYCEGELFDRIVSKG 120
DB 61 KLVCREDEYDVWREIQIMHLSHPNVVRKGYEDSVFVHIVMEYCEGELFDRIVSKG 120
QY 121 HFSERAVKLIKTLGVVACHSLGVNHRDLKPNFLFSPKDDAKLKATDFGLSVFYKP 180
DB 121 HFSERAVKLIKTLGVVACHSLGVNHRDLKPNFLFSPKDDAKLKATDFGLSVFYKP 180
QY 181 ----- 180
DB 181 GLIFLFWLDSLILQLVFWLFPVFSMNRKLNKQSGFLIETGLLFCFIWIANRNVGMVRFDD 240
QY 181 --GOYLYDVGGPYVAPEVKKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQI 238
DB 241 LFGQYLYDVGGPYVAPEVKKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQI 300
QY 239 LQGLDFKSDPWPPTISEAAKDLIYKMLSPKRRISAHEALCHPWIVDQAAAPDKPLDPA 298
DB 301 LQGLDFKSDPWPPTISEAAKDLIYKMLSPKRRISAHEALCHPWIVDQAAAPDKPLDPA 360
QY 299 VLSRLKQFSQMNKIKMALRVIAERLSEEBIGGLKELFKWIDTNSGTTITFEELKAGLKR 358

RESULT 4

Q38869 PRELIMINARY; PRT; 501 AA.
AC Q38869;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE Calmodulin-domain protein kinase CDPK isoform 4 (fragment).
GN CPK4 OR T25922.10 OR AT4G09570.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA McCombie W.R.;
RT "Arabidopsis thaliana Genomic Sequence, Chromosome IV.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA McCombie R.W., Spiegel L.A., Huang E.N., Nascimento L.U.,
RA de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R.,
RA O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H.,
RA Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K.,
RA Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,
RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,
RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U31752; AAB03243.1; -;
DR EMBL; AL161831; CAB8124.1; -;
DR EMBL; AL161515; CAB78080.1; -;
DR HSSP; P02593; 1FW4.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_Thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00054; EFH; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
SQ SEQUENCE 501 AA; 56416 MW; C709C17DFAF74B70 CRC64;


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Query Match          94.8%; Score 2458; DB 10; Length 501;
Best Local Similarity 94.8%; Pred. No. 9.3e-177;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

QY 4 KPNRPSTNVLPTOTPRLRDHYLGKLGQOGFGTTLCTEKSTSNACKSIIPKRLV 63
DB 3 KPNRPSTNVLPTOTPRLRDHYLGKLGQOGFGTTLCTEKSTSNACKSIIPKRLV 62
QY 64 CREDYEDVREIQIMHLSSEHPNVVRIKGTVEDSVFVHIVMEVCEGGEFDRIVSKGHFS 123
DB 63 CREDYEDVREIQIMHLSSEHPNVVRIKGTVEDSVFVHIVMEVCEGGEFDRIVSKGHFS 122
QY 124 EREAUKLTKTILGVVEACHSLGVMRDLKPNFLFDSPKDDAKLKATDFGLSVFKPGQY 183
DB 123 EREAUKLTKTILGVVEACHSLGVMRDLKPNFLFDSPKDDAKLKATDFGLSVFKPGQY 182
QY 184 LYDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQLQSKI 243
DB 183 LYDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQLQSKI 242
QY 244 DFKSDPWPPTISEAAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL SRL 303
DB 243 DFKSDPWPPTISEAAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL SRL 302
QY 304 KQFSOMNKIKKALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSEL 363
DB 303 KQFSOMNKIKKALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSEL 362
QY 364 MESEIKSLMDAADINDSGTIDYGEFLAATLHMNMEREELVAAFSDFDKGSGYITIDE 423
DB 363 MESEIKSLMDAADINDSGTIDYGEFLAATLHMNMEREELVAAFSDFDKGSGYITIDE 422
QY 424 LQACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMKNLNFNIA 483
DB 423 LQACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMKNLNFNIA 482
QY 484 DAFGVG---EKSDD 495
DB 483 EAFGVEDTSSTAKSDD 498

RESULT 5
O24430 ID O24430 PRELIMINARY; PRT; 490 AA.
AC O24430;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE Calmodulin-like domain protein kinase isoenzyme beta.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RN [2]
RP SEQUENCE FROM N.A.
RA McKendree W.L., Doostdar H., McCollum T.G., Mayer R.T.;
RT "cDNA cloning and expression of a gene (Accession No. Z97064) from
RT Citrus paradisi roots similar to bacterial YRN1 and HEAH10 proteins
RT and an mRNA from Brassica oleracea that is wound and dark inducible
RT (PGR97-127).";
RL Plant Physiol. 115:314-314 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Lee J.-Y., Yoo B.-C., Harmon A.C.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U69173; AAB80692.1; -.
DR HSSP; P02588; 1PON
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
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Pfam; PF00069; pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S-TKc; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 490 AA; 55164 MW; 2333C411CAA43E0F CRC64;

Query Match          78.3%; Score 2030; DB 10; Length 490;
Best Local Similarity 81.1%; Pred. No. 1.6e-144;
Matches 386; Conservative 43; Mismatches 45; Indels 2; Gaps 2;

QY 14 VLPQTTPRLRDHYLGKLGQOGFGTTLCTEKSTSNACKSIIPKRLKVCREDYEDVWR 73
DB 12 VLPQTTPRLRDHYLGKLGQOGFGTTLCTEKSTSNACKSIIPKRLKVCREDYEDVWR 71
QY 74 EIQIMHLSSEHPNVVRIKGTVEDSVFVHIVMEVCEGGEFDRIVSKGHFSREAVKLTK 133
DB 72 EIQIMHLSSEHPNVVRIKGTVEDSVFVHIVMEVCEGGEFDRIVSKGHFSREAVKLTK 131
QY 134 ILGVVEACHSLGVMRDLKPNFLFDSPKDDAKLKATDFGLSVFKPGQYLYDVVGSPYY 193
DB 132 ILGVVEACHSLGVMRDLKPNFLFDSPKDDAKLKATDFGLSVFKPGQYLYDVVGSPYY 191
QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQLQSKI 253
DB 192 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQLQSKI 251
QY 254 SEAAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL SRLKQFSOMNKIK 313
DB 252 SEAAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL SRLKQFSOMNKIK 310
QY 314 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELSEIKSLMD 373
DB 311 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELSEIKSLMD 370
QY 374 AADINDSGTIDYGEFLAATLHMNMEREELVAAFSDFDKGSGYITIDE LQSACTEFG 433
DB 371 AADINDSGTIDYGEFLAATLHMNMEREELVAAFSDFDKGSGYITIDE LQSACTEFG 430
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMKNLNFNIA 488
DB 431 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMKNLNFNIA 486
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RESULT 6

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Q93X19 ID Q93X19 PRELIMINARY; PRT; 496 AA.
AC Q93X19;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Calcium dependent protein kinase
DE Calcium dependent protein kinase
GN R1CDPK2.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.
RA Furuichi N., Okita T., Hara N.;
RT "Calcium dependent protein kinase genes from resistant and susceptible
RT potato cultivars to Phytophthora infestans";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB051809; BAB63464.1; -.
DR InterPro; IPR002048; EF-hand.
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RESULT 8
Q9FXQ3 ID Q9FXQ3 PRELIMINARY; PRT; 551 AA.
AC Q9FXQ3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE OsCDPK7.
GN OSCDPK7.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RX MEDLINE=20387027; PubMed=10929125;
RA Saijo Y., Hata S., Kyoizuka J., Shimamoto K., Izui K.;
RT "Over-expression of a single Ca2+-dependent protein kinase confers
RT both cold and salt/drought tolerance on rice plants.";
RL Plant J. 23:319-327(2000).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB042550; BAB16888.1; -.
DR HSSP; P02593; ICTR.
DR Gramene; Q9FXQ3; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; Eph; 4.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00018; EF HAND; 4.
DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 551 AA; 60966 MW; E479A089EF287A7B CRC64;

Query Match 68.4%; Score 1773; DB 10; Length 551;
Best Local Similarity 71.2%; Pred. No. 4.5e-125;
Matches 339; Conservative 53; Mismatches 82; Indels 2; Gaps 2;

QY 13 TVLPYQTPRLRDLHYLLGKLGQGGFGTTLCTEKSSTANYACKSIPKRLKVCREDYEDVW 72
Db 75 SVLGHTPNLRDLHYALGRKLGQGGFGTTLCTELSTGVVDYACKSISKRKLITKEDVDVR 134
QY 73 REIQIMHHLSEHPNVVRIKGTYESVVFHIVMEVCEGGELEFDRIVSKGHFSEREAVKLK 132
Db 135 REIQIMHLSHGKNVVAIKGAYEDQVYVHIVMELCAGGELFDRIIQRGHYSERKAAELTR 194
QY 133 TILGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKQVLYDVVGSYP 192
Db 195 IIVGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKQVLYDVVGSYP 254
QY 193 YVAPVLKCKYGPETDVMSAGVILYLLSGVPPFWAETESGIFRILQGLKDFDKSDPWP 252
Db 255 YVAPVLKCKYGPETDVMSAGVILYLLSGVPPFWAETESGIFRILQGLKDFDKSDPWP 314
QY 253 ISEAADLIYKMLERSPKKRISAEALCHPMIVDEQAAPDKPLDPDAVLSRLKQFSQWNKI 312
Db 315 ISEAKDLITKMLNRPKRLTAHEVLCHPMIRDHGVAADPLDPAVLSRLKQFSQWNKI 374
QY 313 KKMALRVIAELSEEEIGGLKELFMIDTNSGTTTPEELKAGLRKRVGSELMSEIKSLM 372
Db 375 KKMALRVIAELSEEEIAGLMEFQMDADNSGAIITYDELKGLRKYGSTLKTDEIRDL 434
QY 373 DAADIDNSGTIDYGEFLAATLHMNMEREELVAAFSDFDKGSGYITIDELQSACTEFG 432

Db 435 DAADIDNSGTIDYGEFLAATLHMNMEREELVAAFSDFDKGSGYITIDELQSACTEFG 494
QY 433 LCDTPTLDDMIKIDLDNGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIADAFG 487
Db 495 MFDAFLDDVINEADQNDGRIDYGEFVAMMTKGNMGVGR-RTMRNSLNISMRDAPG 549

RESULT 9
O04417 ID O04417 PRELIMINARY; PRT; 492 AA.
AC O04417;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Calcium dependent protein kinase.
GN ZMCDPK1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=honey bantum;
RA Berberich T., Kusano T.;
RT "Cycloheximide induces a subset of low-temperature-inducible genes in
RT maize.";
RL Mol. Gen. Genet. 0:0-0(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97294505; PubMed=9150261;
RA Berberich T., Kusano T.;
RT "Cycloheximide induces a subset of low temperature-inducible genes in
RT maize.";
RL Mol. Gen. Genet. 254:275-283(1997).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; D84408; BAA12338.1; -.
DR HSSP; P02593; ICTR.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; Eph; 4.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00018; EF HAND; 4.
DR PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 492 AA; 54734 MW; 8615C3C3606CE949 CRC64;

Query Match 67.6%; Score 1752; DB 10; Length 492;
Best Local Similarity 70.6%; Pred. No. 1.5e-123;
Matches 334; Conservative 54; Mismatches 83; Indels 2; Gaps 2;

QY 13 TVLPYQTPRLRDLHYLLGKLGQGGFGTTLCTEKSSTANYACKSIPKRLKVCREDYEDVW 72
Db 14 SVLGHTPNLRDLHYALGRKLGQGGFGTTLCTELATGIDYACKSISKRKLITKEDVDVR 73
QY 73 REIQIMHHLSEHPNVVRIKGTYESVVFHIVMEVCEGGELEFDRIVSKGHFSEREAVKLK 132
Db 74 REIQIMHLSHGKNVVAIKGAYEDQVYVHIVMELCAGGELFDRIIQRGHYSERKAAELTR 133
QY 133 TILGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKQVLYDVVGSYP 192
Db 134 IIVGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKQVLYDVVGSYP 193
QY 193 YVAPVLKCKYGPETDVMSAGVILYLLSGVPPFWAETESGIFRILQGLKDFDKSDPWP 252
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Db 194 YVAPEVLLKSYGPAADVWTVAGVILYLLSGVPPFAETQOGIFDAVLKGAIDFSDPWPV 253
QY 253 ISEAAKDLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQWNKI 312
Db 254 ISDSAKDLIRMLNPRPAERLTAHEVLCHPWIRDHGVAPDRPLDPVLSRIKQFSQWNKL 313
QY 313 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELMSEIKSLM 372
Db 314 KQALRVIAERLSEEEIAGLKEMFQMTDNTNSGTTTFEELKAGLRKRVGSELMSEIKSLM 373
QY 373 DAADIINSGTIDYGEFLAATLHNMKMEREEILVAAFSDPKDGSYITIDELQACTEFG 432
Db 374 DAADIINSGTIDYGEFLAATLHNMKMEREEILVAAFSDPKDGSYITIDELQACTEFG 433
QY 433 LCTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIAD 484
Db 434 MPDAFLDDVINEADQNDGRIDYGEFVAMTKGNMGVGR-RTMRSNLINSMRD 485

RESULT 10

Q43676 PRELIMINARY; PRT; 487 AA.
AC Q43676;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Calcium dependent protein kinase.
GN CDPK.
OS Phaseolus aureus (Mung bean) (Vigna radiata).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
OX NCBI_TaxId=3916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=twilcz, and cv. Berken; TISSUE=Etisolated hypocotyl;
RX MEDLINE=96311003; PubMed=8704124; Villa M., Arteca R.N.;
RA Botella J.R., Arteca J.M., Somodevilla M., Arteca R.N.;
RT "Calcium-dependent protein kinase gene expression in response to
physical and chemical stimuli in mungbean (Vigna radiata).";
RL Plant Mol. Biol. 30:1129-1137(1996).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U08140; AAC49405.1; --
DR HSSP; Q63450; 1A06.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR SMART; SM00054; EPH; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 487 AA; 54700 MW; 54E6FBF5D93AEB2 CRC64;

Query Match 67.5%; Score 1751; DB 10; Length 487;
Best Local Similarity 69.1%; Pred. No. 1.7e-123;
Matches 327; Conservative 64; Mismatches 80; Indels 2; Gaps 2;

QY 14 VLPTQTPRLDRHYLLGKLGQOGFGTTYLTCTEKSTSANVACKSIIPKRLVCRDVEDVWR 73
Db 12 VLGHKTPNIRDLYTLGRKLGQOGFGTTYLTCTENSTSNVACKSIKRLISKEDVEDVWR 71
QY 74 EIQIMHHLSEHNVRVRIKTYEDSDVVFVHIVMEVCGGELFDRIVSKGHFSERAEVLIKT 133
Db 72 EIQIMHHLGAKHKNIVITKAGVEDPLYVHIVMELSCGGELFDRIQGHVTERKAAELTKI 131

QY 134 ILGWBEACHSLGVHRLDKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYY 193
Db 132 IVGWBEACHSLGVHRLDKPENFLVKNKDDDFSLKAIKDFGLSVFYKPGQYLYDVVGSPYY 191
QY 194 VAPEVLKCYGPRIDVNSAGVILYLLSGVPPFAETESGIFQIIOGLKDLDFKSDPPTI 253
Db 192 VAPEVLKCYGPRIDVNSAGVILYLLSGVPPFAETQOGIFDAVLKGHIDFSDPMPLI 251
QY 254 SEAAKDLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQWNKI 313
Db 252 SDGSKDLIRMLNPRPAERLTAHEVLCHPWIRDHGVAPDRPLDPVLSRIKQFSQWNKL 311
QY 314 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELMSEIKSLM 373
Db 312 KQALRVIAERLSEEEIAGLRKEMFQMTDNTNSGTTTFEELKAGLRKRVGSELMSEIKSLM 371
QY 374 DAADIINSGTIDYGEFLAATLHNMKMEREEILVAAFSDPKDGSYITIDELQACTEFG 433
Db 372 DAADVDKSGTIDYGEFLAATLHNMKMEREEILVAAFSDPKDGSYITIDELQACTEFG 431
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIAD 485
Db 432 TDAFLEDIIRVDDQNDGRIDYGEFVAMTKGNMGVGR-RTMRSNLINSMRD 483

RESULT 11

Q8LPV8 PRELIMINARY; PRT; 558 AA.
AC Q8LPV8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Calmodulin-like domain protein kinase CPK2.
OC Cucurbita maxima (pumpkin) (Winter squash).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxId=3661;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Big Max;
RX MEDLINE=21975187; PubMed=11847230;
RA Yoo B.C., Lee J.Y., Lucas W.J.;
RT "Analysis of the Complexity of Protein Kinases within the Phloem Sieve
Tube System. CHARACTERIZATION OF CUCURBITA MAXIMA CALMODULIN-LIKE
RT DOMAIN PROTEIN KINASE 1.";
RL J. Biol. Chem. 277:15325-15332(2002).
DR EMBL; AY072802; AAL68972.1; --
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EPH; 4.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 558 AA; 62526 MW; 4D62EB5D74F516B CRC64;

Query Match 67.3%; Score 1746; DB 10; Length 558;
Best Local Similarity 69.5%; Pred. No. 5e-123;
Matches 330; Conservative 59; Mismatches 84; Indels 2; Gaps 2;

QY 14 VLPTQTPRLDRHYLLGKLGQOGFGTTYLTCTEKSTSANVACKSIIPKRLVCRDVEDVWR 73
Db 83 VLGHKTPNIRDLYTLGRKLGQOGFGTTYLTCTEIMTGIEYACKSIKRLIAKEDVEDVRR 142

Qy 74 EIQMHLSHPNVVRKGTIEDSVFVHVMVECEGGELFDRIVSKGHFSREAVKLIK 133
 Db 143 EIQMHLSHPNVVRKGTIEDSVFVHVMVECEGGELFDRIVSKGHFSREAVKLIK 202
 Qy 134 ILGVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193
 Db 203 ILGVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 262
 Qy 194 VAPEVLKCYGPEIDVMSAGVILYLLSGVPPFPAETESGIFRILQGLKDFKSDPMTI 253
 Db 263 VAPEVLKCYGPEIDVMSAGVILYLLSGVPPFPAETESGIFRILQGLKDFKSDPMTI 322
 Qy 254 SEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSOMNKK 313
 Db 323 SDSAKDLIRKMLCRSPDRDLTAHEVLCHPWICENGVAAPDRALDPAVLSRLKQFSOMNKK 382
 Qy 314 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVGSSELMSEIKSLMD 373
 Db 383 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVGSSELMSEIKSLMD 442
 Qy 374 AADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKGSGYITIDELQSACTEFG 433
 Db 443 AADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKGSGYITIDELQSACTEFG 502
 Qy 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRRTMMKNLNFNIADAFG 487
 Db 503 TDAYLEIIRVDDQNDGRIDYSEFVAMMOKGNAGIGR-RTMRNSLNSMRDGP 556

RESULT 12

O04123 ID O04123 PRELIMINARY; PRT; 554 AA.
 AC O04123;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Calcium-dependent protein kinase.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=inbred line H84;
 RX MEDLINE=97201047; PubMed=9048876;
 RA Saijo Y., Hata S., Sheen J., Izui K.;
 RT "cDNA cloning and prokaryotic expression of a maize calcium-dependent
 protein kinase".
 RL Biochim. Biophys. Acta 1350:109-114(1997).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; D87042; BAA13232.1; -;
 DR HSSP; P02593; 1CTR.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR000719; Prot_kinase.
 DR InterPro; IPR002290; Ser_Thr_kinase.
 DR Pfam; PF00036; ehand; 4.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000012; EF-hand; 2.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR SMART; SM00054; EFh; 4.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00018; EF_HAND; 4.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 554 AA; 61056 MW; 51FC6F4684C57C6 CRC64;

Query Match 67.3%; Score 1745; DB 10; Length 554;
 Best Local Similarity 70.0%; Pred. No. 5.9e-123;
 Matches 333; Conservative 57; Mismatches 84; Indels 2; Gaps 2;

Qy 13 TVLPYOTPLRDHYLLGKLGOGGFTTYLCTEKSTSANVACKSIKKRLVCREDYEDVM 72
 Db 78 SVLGHPTPNURDLYALGRKLGOGGFTTYLCTELATGVYACKSISKKRLITREDVDDVR 137
 Qy 73 REIQMHLSHPNVVRKGTIEDSVFVHVMVECEGGELFDRIVSKGHFSREAVKLIK 132
 Db 138 REIQMHLSHPNVVRKGTIEDSVFVHVMVECEGGELFDRIVSKGHFSREAVKLIK 197
 Qy 133 TIIGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 192
 Db 198 TIIGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 257
 Qy 193 YVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFPAETESGIFRILQGLKDFKSDPMTI 252
 Db 258 YVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFPAETESGIFRILQGLKDFKSDPMTI 317
 Qy 253 ISAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSOMNKK 312
 Db 318 ISDSAKDLIRKMLCRSPDRDLTAHEVLCHPWICENGVAAPDRALDPAVLSRLKQFSOMNKK 377
 Qy 313 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVGSSELMSEIKSLMD 372
 Db 378 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVGSSELMSEIKSLMD 437
 Qy 373 DAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKGSGYITIDELQSACTEFG 432
 Db 438 DAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKGSGYITIDELQSACTEFG 497
 Qy 433 LCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRRTMMKNLNFNIADAFG 487
 Db 498 MPDAFLDDVINEADQNDGRIDYGEFVAMMOKGNAGIGR-RTMRNSLNSMRDGP 552

RESULT 13
 Q38871 ID Q38871 PRELIMINARY; PRT; 556 AA.
 AC Q38871;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Calmodulin-domain protein kinase CDPK isoform 5.
 GN CPK5 OR P23B12.130 OR AT4G35310.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Hrabak E.M., Dickmann L.J., Satterlee J.S., Sussman M.R.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
 RA Hoheisel J., Jesse T., Heijnen L., Vos P., Mewes H.W., Mayer K.F.X.,
 RA Schueller C.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,
 RA Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL; U31834; AAB03245.1; -;
 DR EMBL; AL022604; CAA18738.1; -;
 DR EMBL; AL161587; CAB80248.1; -;
 DR HSSP; P02588; 1TNX.

```
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 556 AA; 62127 MW; 737F1ADD582B45ED CRC64;

Query Match 67.2%; Score 1742; DB 10; Length 556;
Best Local Similarity 68.4%; Pred. No. 1e-122;
Matches 329; Conservative 66; Mismatches 84; Indels 2; Gaps 2;

QY 6 NRRPSNTVLVPTQPLRDHYLLGKLGQGGTTLCTEKSTSYACKSIPKRLVCR 65
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
77 NPDNQAYVVGKTNIRDIYTLRSKLGQGGTTLCTEIASGVYACKSISKRLISK 136
QY 66 EDYEDVWREIQIMHLSHPNVVRIKGYEDSVFVHIVMEVCEGELFDRIIVSKGHPSE 125
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
137 EDVEDVREIQIMHLSHPNVVRIKGYEDSVFVHIVMEVCEGELFDRIIVSKGHPSE 196
QY 126 EAVKLITKILGVVEACHSLGVNHRDLKPENFLFDSPKDDAKLKATDFGLSVFYPKQVLY 185
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
197 KAAELTKIIVGVVEACHSLGVNHRDLKPENFLFVNNKDDDFSLKIDFGLSVFYPKQVLY 256
QY 186 DVVGSPPYVAPEVLKCKYGEIDVMSAGVILYLLSGVPPVWAEETSGIFRQILQGLDF 245
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
257 DVVGSPPYVAPEVLKRYGPEADVMTAGVILYLLSGVPPVWAEETQGGIFDAVLKGYIDF 316
QY 246 KSDPWPPTISEAAKLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLPAVLRLKQ 305
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
317 ESDPWPVLSDAKLIIRMLSKPAERLTAHEVLRHPWICENGVAAPDALPAPVLRLKQ 376
QY 306 FSQMKIKKMLRVIAERLSBEEIIGGLKELFKMIDTNSGTTTFBELKAGLRKVGSELME 365
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
377 FSAMNKKKMLKVIAESLSBEEIAGLRKVGSELMEQAMDTNSGTTTFBELKAGLRKVGSTLKD 436
QY 366 SEIKSLMDAADIDNSGTTIDYGEFLAATLHMNMEREELVAAFSDFDKDGGYITIDELQ 425
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
437 TEIHLMDAADVNSGTTIDYSEFTAATLHNLKEREELVAAFAQYFDKDGSGFTIDELQ 496
QY 426 SACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRMTMMKLNFNIA 484
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
497 QACVEHGNADVFLIEDIIKEVDQNDGKIDYGEFVEMMQGNAGVGR-RTMRSNLSNMRD 555

QY 485 A 485
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
556 A 556

RESULT 14
Q93XJ0 Q93XJ0 PRELIMINARY; PRT; 578 AA.
AC Q93XJ0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Calcium dependent protein kinase.
GN RICDPK1.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=sv. Rishiri;
RA Furuichi N., Okuta T., Hara N.;
RT "Calcium dependent protein kinase genes from resistant and susceptible
RL potato cultivars to Phytophthora infestans";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB051808; BAB63463.1; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 578 AA; 64779 MW; 1009FF973EB662D2 CRC64;

Query Match 67.1%; Score 1739.5; DB 10; Length 578;
Best Local Similarity 67.6%; Pred. No. 1.6e-122;
Matches 326; Conservative 62; Mismatches 79; Indels 15; Gaps 1;

QY 2 ETKPNRPP-----SNTVLPYQTPRLRDHYLLGKLGQGGTTLCTEK 46
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
75 EEQPPKPKPKPAEMKRVSSAGRLTDSVLQKKTGNLKEFFSIGRKLGGQGGTTFKCEVK 134
QY 47 STSANYACKSIPKRLVCREDYEDVWREIQIMHLSHPNVVRIKGYEDSVFVHIVMEV 106
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
135 ATGKEYACKSIAKRLKLLTDDDDVEDVRREVQIMHLAGHPHVISIKGAYEDAVAVHVMVF 194
QY 107 CEGELFDRIIVSKGHFSEREAVKLIKILGVVEACHSLGVNHRDLKPENFLFDSPKDDAK 166
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
195 CAGGELFDRIIQRGHYTERKAAELTRITVGVVEACHSLGVNHRDLKPENFLFVQDKEDSL 254
QY 167 LKATDFGLSVYPKQVLYDVVGSPPYVAPEVLKCKYGEIDVMSAGVILYLLSGVPPF 226
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
255 LKADFGLSIFPKPGDFTDVVGSPPYVAPEVLKRYGPEADVMSAGVILYLLSGVPPF 314
QY 227 WAETESGIFRQILQGLDFKSDPWPPTISEAAKLIYKMLERSPKKRISAHEALCHPWIVD 286
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
315 WAENEQGIQEVLGAGLDLDFKSDPWPSPSEDAKLMRLMLVDRPRLTAHEVLCHPNVQV 374
QY 287 EQAAPDKPLDPAVLRLSKQFSQMNKIKKMLRVIAERLSBEEIIGGLKELFKMIDTNSGT 346
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
375 DGVAPDKPLDSAVLSRMKQFSAMNKKKMLRVIAESLSBEEIAGLKEMFKMIDTNSGQ 434
QY 347 ITFBEELKAGLRKVGSELMESEIKSLMDAADIDNSGTTIDYGEFLAATLHMNMEREELV 406
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
435 ITFBEELKAGLRKFGSNLKEITEIYDLMDAADVNSGTTIDYGEFIAATLHMNKIERQDHLFA 494
QY 407 AFSDFDKGGSYITIDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD 466
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
495 AFCYFDKGGSYITADELQACEFGIGDVMEEMIREADQNDQNDGRIDYNEFVAMMQGN 554
QY 467 GV 468
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : :
555 PV 556

RESULT 15
Q8LPV9 Q8LPV9 PRELIMINARY; PRT; 571 AA.
AC Q8LPV9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Phloem calmodulin-like-domain protein kinase PCPK1.
OS Cucurbita maxima (Pumpkin) (Winter squash).
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 10:31:21 ; Search time 81 Seconds
(without alignments)
969.996 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPNTVLPYQTP.....KNLNFNTADAFVGDEKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2593	100.0	495	23	Arabidopsis CDPK2
2	2458	94.8	501	21	Arabidopsis thalia
3	2458	94.8	501	23	Arabidopsis CDPK4
4	2064	79.6	425	21	Arabidopsis thalia
5	1932	74.5	512	20	Soybean CDPK prote
6	1924	74.2	399	21	Arabidopsis thalia
7	1742	67.2	483	21	Arabidopsis thalia
8	1742	67.2	556	21	Arabidopsis thalia
9	1703	65.7	856	21	Arabidopsis thalia

10	1703	65.7	893	21	AAG38598	Arabidopsis thalia
11	1703	65.7	1017	21	AAG38597	Arabidopsis thalia
12	1672.5	64.5	639	23	ABP53637	Maize calcium depe
13	1509.5	58.2	549	23	AAM52842	Physcomitrella pat
14	1509	58.2	408	21	AAG31159	Arabidopsis thalia
15	1501	57.9	463	21	AAG46565	Arabidopsis thalia
16	1500	57.8	280	22	AAG65758	ATCDPK2 kinase dom
17	1462	56.4	529	21	AAG29590	Arabidopsis thalia
18	1462	56.4	542	21	AAG29589	Arabidopsis thalia
19	1460.5	56.3	459	21	AAG29591	Arabidopsis thalia
20	1457	56.2	569	15	AAR56237	Protein kinase spe
21	1325.5	51.1	538	21	AAG43621	Arabidopsis thalia
22	1319	50.9	404	21	AAG46566	Arabidopsis thalia
23	1231	47.5	378	21	AAG46567	Arabidopsis thalia
24	1187.5	45.8	307	20	AAW93255	Tobacco CDPK prote
25	1166.5	45.0	424	21	AAG43622	Arabidopsis thalia
26	1153.5	44.5	421	21	AAG43623	Arabidopsis thalia
27	1059	40.8	413	22	AAG65755	ATCDPK kinase doma
28	1015.5	39.2	523	21	AAG10101	Arabidopsis thalia
29	928.5	35.8	426	21	AAG10102	Arabidopsis thalia
30	920.5	35.5	302	21	AAG54428	Zea mays protein f
31	900	34.7	274	22	AAG5756	ATCDPK1 kinase dom
32	887	34.2	274	19	AAW49837	Amino acid sequenc
33	887	34.2	274	22	AAG65757	ATCDPK1a kinase do
34	887	34.2	274	22	AAG65759	ATCDPK1a PK domain
35	849	32.7	597	23	AAM52841	Physcomitrella pat
36	842.5	32.5	384	21	AAG10103	Arabidopsis thalia
37	829	32.0	623	22	AAB55583	Rice CDPK (clone r
38	829	32.0	623	23	ABP53630	Maize calcium depe
39	826	31.9	625	23	ABP53638	Maize calcium depe
40	800	30.9	576	23	ABP53639	A. thaliana calciu
41	771.5	29.8	456	16	AAR74996	E. maxima Em70-1 a
42	753.5	29.1	504	21	AAG16593	Arabidopsis thalia
43	753.5	29.1	594	21	AAG16592	Arabidopsis thalia
44	737	28.4	502	21	AAG33884	Arabidopsis thalia
45	737	28.4	594	21	AAG53883	Arabidopsis thalia

ALIGNMENTS

RESULT 1
AAM48000
ID AAM48000 standard; Protein; 495 AA.
XX AAM48000;
XX AC
XX DT 08-MAR-2002 (first entry)
XX DE
XX DE Arabidopsis CDPK2 SEQ ID NO 1.
XX KW Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed;
XX KW disease resistance; agricultural; pathogen; crop yield; ornamental;
XX KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;
XX KW transgenic; plant; enzyme.
XX OS Arabidopsis thaliana.
XX PN WO200184911-A1.
XX PD 15-NOV-2001.
XX PF 04-MAY-2001; 2001WO-US14368.
XX PR 05-MAY-2000; 2000US-201925P.
XX PA (GEO) GEN HOSPITAL CORP.
XX PI Sheen J;
XX DR WPI; 2002-062179/08.
XX DR N-PSDB; ABA06021.
XX

PT Producing plant having increased disease resistance, comprises
PT regenerating plant from a non-naturally occurring plant cell
PT over-expressing a polynucleotide encoding a calcium dependent protein
XX kinase polypeptide
XX
XX Disclosure; Fig 1; 44pp; English.
XX
CC The invention relates to producing a plant having increased disease
CC resistance, comprising providing a non-naturally occurring plant cell
CC over-expressing a polynucleotide encoding a calcium dependent protein
CC kinase (CDPK) polypeptide and regenerating a plant from the plant
CC cell, where the CDPK polypeptide is expressed in the plant, increasing
CC the resistance of the plant to disease as compared to a
CC naturally-occurring plant. The method is useful for a variety of
CC agricultural and commercial purposes including improving a plant's
CC resistance against plant pathogens, increasing crop yields, improving
CC crop and ornamental quality and reducing agricultural production costs.
CC The method facilitates an effective and economical method for in-plant
CC protection against plant pathogen, reducing or minimising the need for
CC traditional chemical practices (e.g. application of fungicides,
CC bactericides, nematocides, insecticides, or viricides) that are typically
CC used by farmers for controlling the spread of plant pathogens and
CC providing protection against disease causing pathogens. The method
CC contributes to the production of high quality and high yield agricultural
CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops
CC having reduced spots, blemishes and blotches that are caused by
CC pathogens, agricultural products with increased shelf-life and reduced
CC handling costs and high quality and yield crops for agricultural
CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial
CC (e.g. fiber crops) purposes. The present sequence is that of Arabidopsis
CC thaliana CDPK2 of the invention.
XX
XX Sequence 495 AA;

Query Match 100.0%; Score 2593; DB 23; Length 495;
Best Local Similarity 100.0%; Pred. No. 2.2e-222;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 METKENRRPSNTVL PYQTPRLRDHYLLGKLGQGGQGTLYLCTEKSTSANVACKSIPIKR 60
DB 1 METKENRRPSNTVL PYQTPRLRDHYLLGKLGQGGQGTLYLCTEKSTSANVACKSIPIKR 60
QY 61 KLVCREDYEDVWREIQIMHLLSEHPNVVRIKGTYESDVFVHIVMEVCEGGELFDRIVSKG 120
DB 61 KLVCREDYEDVWREIQIMHLLSEHPNVVRIKGTYESDVFVHIVMEVCEGGELFDRIVSKG 120
QY 121 HFSEREAVKLITKILGVVEACHSLGVHRLDKPENFLFDSPKDDAKLKATDFGLSVFYKP 180
DB 121 HFSEREAVKLITKILGVVEACHSLGVHRLDKPENFLFDSPKDDAKLKATDFGLSVFYKP 180
QY 181 GOYLYDVVGVSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
DB 181 GOYLYDVVGVSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240
QY 241 GKLFKSPDPWTISEAAKDLTKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVL 300
DB 241 GKLFKSPDPWTISEAAKDLTKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVL 300
QY 301 SRLKQFSQNNKIKKMLRVIAERISEEIGGKELFKMIDTNSGTITFEELKAGLKEVG 360
DB 301 SRLKQFSQNNKIKKMLRVIAERISEEIGGKELFKMIDTNSGTITFEELKAGLKEVG 360
QY 361 SELMESEIKSLMDAADINSGTIDYGEFLAATLHNNKEREELVAAPDFDKDGSYIT 420
DB 361 SELMESEIKSLMDAADINSGTIDYGEFLAATLHNNKEREELVAAPDFDKDGSYIT 420
QY 421 IDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMVRKGDGVGRSRTMMKNLNF 480
DB 421 IDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMVRKGDGVGRSRTMMKNLNF 480
QY 481 NIADAFGVGDKSDD 495
DB 481 NIADAFGVGDKSDD 495

RESULT 2
AAG35776
ID AAG35776 standard; Protein; 501 AA.
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XX AAG35776;
XX
XX 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 43753.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
XX
XX 09-MAR-1999; 99US-0123180.
XX
XX 23-MAR-1999; 99US-0123548.
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XX 25-MAR-1999; 99US-0135788.
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XX 29-MAR-1999; 99US-0126264.
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XX 01-APR-1999; 99US-0126785.
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XX 06-APR-1999; 99US-0127462.
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XX 08-APR-1999; 99US-0128234.
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XX 16-APR-1999; 99US-0128714.
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XX 19-APR-1999; 99US-0129845.
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XX 28-MAY-1999; 99US-0136392.
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PR 18-AUG-1999; 99US-0149426.

PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 21-OCT-1999; 99US-0160767.
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PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 94.8%; Score 2458; DB 21; Length 501;
Best Local Similarity 94.8%; Pred. No. 2.4e-210;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

Qy 4 KPNRRPSNTVLPYQTRLRDRHYLLGKLGQGGTGYLCTCKEKSANYACKSIPKRLV 63
Db 3 KPNRRPSNSVLPYETRLRDRHYLLGKLGQGGTGYLCTCKEKSANYACKSIPKRLV 62
Qy 64 CREDYEDVWREIQIMHHLSEHPNVVRIRKGTVEDSVFVHIWMEVCEGGELFDRIVSKGHFS 123
Db 63 CREDYEDVWREIQIMHHLSEHPNVVRIRKGTVEDSVFVHIWMEVCEGGELFDRIVSKGCFS 122
Qy 124 EREAVKLIKTLGVVEACHSLGVNMRDLKPNFLFDSPKDDAKLKATDFGLSVFYKFGQY 183
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Db 123 EREAALIKITILGVVEACHSLGVNHRDLKPENFLFSDDAKLKATDFGLSVFYKPGQY 182
Qy 184 LYDVVGSPPYVAPEVLKCCYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLK 243
Db 183 LYDVVGSPPYVAPEVLKCCYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLK 242
Qy 244 DFKSDPWTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAADPKPLDPAVLRL 303
Db 243 DFKSDPWTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAADPKPLDPAVLRL 302
Qy 304 KQFSQMKIKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKVGSEL 363
Db 303 KQFSQMKIKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKVGSEL 362
Qy 364 MESEIKSLMDAADIDNSGTTIDYGFLLAATLHMKNWEEELVAAFSDFDKDGSYITIDE 423
Db 363 MESEIKSLMDAADIDNSGTTIDYGFLLAATLHMKNWEEELVAAFSDFDKDGSYITIDE 422
Qy 424 LOSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKKGDGVRGRSRTMMKNLNFNIA 483
Db 423 LOOACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKKGDGVRGRSRTMMKNLNFNIA 482
Qy 484 DAFGVDG----EKSDD 495
Db 483 EAFGVEDTSSTAKSDD 498

RESULT 3

AAM48001
ID AAM48001 standard; Protein; 501 AA.

XX AC AAM48001;

XX DT 08-MAR-2002 (first entry)

XX DE Arabidopsis CDPK4 SEQ ID NO 3.

XX KW Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed;
XX KW disease resistance; agricultural; pathogen; crop yield; ornamental;
XX KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;
XX KW transgenic; plant; enzyme.

XX OS Arabidopsis thaliana.

XX PN WO200184911-A1.

XX PD 15-NOV-2001.

XX PF 04-MAY-2001; 2001WO-US14368.

XX PR 05-MAY-2000; 2000US-201925P.

XX PA (GEO) GEN HOSPITAL CORP.

XX PI Sheen J;

XX DR WPI; 2002-062179/08.

XX DR N-PSDB; ABA06022.

XX PT Producing plant having increased disease resistance, comprises
XX PT regenerating plant from a non-naturally occurring plant cell
XX PT over-expressing a polynucleotide encoding a calcium dependent protein
XX PT kinase polypeptide

XX PS Disclosure; Fig 2; 44pp; English.

XX CC The invention relates to producing a plant having increased disease
XX CC resistance, comprising providing a non-naturally occurring disease
XX CC over-expressing a polynucleotide encoding a calcium dependent protein
XX CC kinase (CDPK) polypeptide and regenerating a plant from the plant
XX CC cell, where the CDPK polypeptide is expressed in the plant, increasing
XX CC the resistance of the plant to disease as compared to a
XX CC naturally-occurring plant. The method is useful for a variety of

CC agricultural and commercial purposes including improving a plant's
CC resistance against plant pathogens, increasing crop yields, improving
CC crop and ornamental quality and reducing agricultural production costs.
CC The method facilitates an effective and economical method for in-plant
CC protection against plant pathogen, reducing or minimising the need for
CC traditional chemical practices (e.g. application of fungicides,
CC bactericides, nematocides, insecticides, or viricides) that are typically
CC used by farmers for controlling the spread of plant pathogens and
CC providing protection against disease causing pathogens. The method
CC contributes to the production of high quality and high yield agricultural
CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops
CC having reduced spots, blemishes and blotches that are caused by
CC pathogens, agricultural products with increased shelf-life and reduced
CC handling costs and high quality and yield crops for agricultural
CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial
CC (e.g. fiber crops) purposes. The present sequence is that of Arabidopsis
CC thaliana CDPK4 of the invention.

XX SQ Sequence 501 AA;

Query Match 94.8%; Score 2458; DB 23; Length 501;
Best Local Similarity 94.8%; Pred. No. 2.4e-210;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

Qy 4 KPNRPSPNTVLPYQTPRLRDHYLLGKLGQGGFGTTYLCTEKSTSANVACKSIPKRLV 63
Db 3 KPNRPSPNSVLPYETPRLRDHYLLGKLGQGGFGTTYLCTEKSSANVACKSIPKRLV 62
Qy 64 CREDYEDVWREIQIMHHLSEHPNVVRIKGTYESVVFVHIVMEVCEGELFDRIVSKGHS 123
Db 63 CREDYEDVWREIQIMHHLSEHPNVVRIKGTYESVVFVHIVMEVCEGELFDRIVSKGFS 122
Qy 124 EREAVALIKITILGVVEACHSLGVNHRDLKPENFLFSDDAKLKATDFGLSVFYKPGQY 183
Db 123 EREAVALIKITILGVVEACHSLGVNHRDLKPENFLFSDDAKLKATDFGLSVFYKPGQY 182

Qy 184 LYDVVGSPPYVAPEVLKCCYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLK 243
Db 183 LYDVVGSPPYVAPEVLKCCYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLK 242
Qy 244 DFKSDPWTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAADPKPLDPAVLRL 303
Db 243 DFKSDPWTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAADPKPLDPAVLRL 302

Qy 304 KQFSQMKIKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKVGSEL 363
Db 303 KQFSQMKIKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKVGSEL 362

Qy 364 MESEIKSLMDAADIDNSGTTIDYGFLLAATLHMKNWEEELVAAFSDFDKDGSYITIDE 423
Db 363 MESEIKSLMDAADIDNSGTTIDYGFLLAATLHMKNWEEELVAAFSDFDKDGSYITIDE 422

Qy 424 LOSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKKGDGVRGRSRTMMKNLNFNIA 483
Db 423 LOOACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKKGDGVRGRSRTMMKNLNFNIA 482

Qy 484 DAFGVDG----EKSDD 495
Db 483 EAFGVEDTSSTAKSDD 498

RESULT 4

AAG35777

ID AAG35777 standard; Protein; 425 AA.

XX AC AAG35777;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 43754.

XX KW Protein identification; signal transduction pathway; metabolic pathway;
XX KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.
XX Arabidopsis thaliana.
XX EP1033405-A2.
XX PD 06-SEP-2000.
XX XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
XX 05-MAR-1999; 99US-0123180.
XX 09-MAR-1999; 99US-0123548.
XX 23-MAR-1999; 99US-0125788.
XX 25-MAR-1999; 99US-0126264.
XX 29-MAR-1999; 99US-0126785.
XX 01-APR-1999; 99US-0127462.
XX 06-APR-1999; 99US-0128234.
XX 08-APR-1999; 99US-0128714.
XX 16-APR-1999; 99US-0129845.
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XX 04-MAY-1999; 99US-0132484.
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XX 22-JUN-1999; 99US-0139899.
XX 23-JUN-1999; 99US-0140353.
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XX 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
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PR 08-JUL-1999; 99US-0142803.
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PR 09-AUG-1999; 99US-0147935.
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PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
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PR 26-AUG-1999; 99US-0150884.
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PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 31-AUG-1999; 99US-0151303.
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PR 07-SEP-1999; 99US-0151930.
PR 99US-0152263.

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PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 14-OCT-1999; 99US-0159330.
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PR 18-OCT-1999; 99US-0159584.
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PR 22-OCT-1999; 99US-0160980.
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PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 79.6%; Score 2064; DB 21; Length 425;
Best Local Similarity 94.5%; Pred. No. 2,7e-175;
Matches 399; Conservative 6; Mismatches 13; Indels 4; Gaps 1;

QY 78 MHHLSEHPNVVRIGTGYEDSVFVHIVMEVCEGGELEFDRIVSKGHFSREAVKLIKILGV 137
DB 1 MHHLSEHPNVVRIGTGYEDSVFVHIVMEVCEGGELEFDRIVSKGHFSREAAKLIKILGV 60

QY 138 VEACHSLGVNHRDLKPENFLFDSPPKODAKLKATDFGLSVFYKPGQYLYDVVGGPYVAPE 197
DB 61 VEACHSLGVNHRDLKPENFLFDSPPKODAKLKATDFGLSVFYKPGQYLYDVVGGPYVAPE 120

QY 198 VLKCKYGEPEIDVNSAGVILYLLSGVPPFWAETESGIFRQILOQKLDKSDPWTISEAA 257
DB 121 VLKCKYGEPEIDVNSAGVILYLLSGVPPFWAETESGIFRQILOQKLDKSDPWTISEGA 180

QY 258 KDLIYKMLRSPKKRISAEALCHPMIVDEOAAPEKPLDPAVLRLKQFSQMKIKQMAL 317
DB 181 KDLIYKMLRSPKKRISAEALCHPMIVDEOAAPEKPLDPAVLRLKQFSQMKIKQMAL 240

QY 318 RVIAERLSEBEIGGLKELFKMIDTNSGTTTFEELKAGLRKVGSELMESEIKSLMDAADI 377
DB 241 RVIAERLSEBEIGGLKELFKMIDTNSGTTTFEELKAGLRKVGSELMESEIKSLMDAADI 300

QY 378 DMSGTIDYGEFLAATLHMKMEREELVAAFSDFDKDGGGYITIDELQSACTEFGLCDTP 437
DB 301 DMSGTIDYGEFLAATLHMKMEREENLVAAFSDFDKDGGGYITIDELQSACTEFGLCDTP 360
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QY 438 LDDMIKEIDLNDGKIDFSEFTAMMRKGGVGRSRTMMKNLNFNIADAFGVDG---EKS 493
DB 361 LDDMIKEIDLNDGKIDFSEFTAMMRKGGVGRSRTMMKNLNFNIADAFGVDG---EKS 420
QY 494 DD 495
DB 421 DD 422

RESULT 5
AAW93256
ID AAW93256 standard; Protein; 512 AA.
XX
AC AAW93256;
XX
DT 25-AUG-1999 (first entry)
XX
DE Soybean CDPK protein.
XX
KW CDPK; calcium dependent protein kinase; tobacco; pathogen; invasion;
KW induction; elicitor; plant; disease resistance; parasiticide; soybean;
KW elicitor.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT Region 41..46
FT /note= "protein kinase sequence"
FT Region 158..163
FT /note= "protein kinase sequence"
FT Region 198..205
FT /note= "protein kinase sequence"
FT Binding-site 348..360
FT /note= "calcium binding site"
FT Binding-site 388..399
FT /note= "calcium binding site"
FT Binding-site 425..435
FT /note= "calcium binding site"
FT Binding-site 458..468
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XX
PN WO9902655-A1.
XX
PD 21-JAN-1999.
XX
PF 07-JUL-1998; 98WO-US14109.
XX
PR 08-JUL-1997; 97US-0889655.
XX
PA (KENT ) UNIV KENTUCKY RES FOUND.
XX
PI Chappell J, Lusso MFG;
XX
DR WPI; 1999-120859/10.
XX
PT New polynucleotides based on calcium dependent protein kinase genes
XX - useful to induce disease resistance in plants
XX
PS Example 4; Fig 4; 51pp; English.
XX
CC This invention describes a novel nucleic acid molecule and its encoded
CC protein that are induced upon pathogen invasion or elicitor treatment.
CC The products of the invention are functional in plants, plant tissue and
CC in plant cells for inducible gene expression and altering the disease
CC resistance phenotype of plants. The products of the invention are
CC related to calcium dependent protein kinase (CDPK) genes. The invention
CC describes the isolation of a novel tobacco CDPK protein fragment and its
CC encoding nucleic acid, isolated from a cell suspension culture derived
CC from a tobacco cultivar KY14 explant, after growth in the presence of
CC the elicitor parasiticide. This sequence represents the soybean CDPK
CC protein which is used in the description of the method.
XX
SQ Sequence 512 AA;
```

Query Match	74.5%	Score 1932	DB 20	Length 512
Best Local Similarity	77.1%	Pred. N.2.le-163		
Matches 370	Conservative 51	Mismatches 51	Indels 8	Gaps 4
QY	14	VLPYOTPLRDHYLLGKLGQOGFGTTVLTCTEKSTSANVACKSIIPKRLKLVCREDEDVNR	73	
DB	22	VLPQRTQNIREVVEYGRKLGQOGFGTTCTRAGSGGFACKSIIPKRLCKCKEDVEDVNR	81	
QY	74	EIQIMHILSEHPNVRIKGTVEYDSVFVHIVMEVCEGGELFDRIVSKGHFSEREAVLKIKT	133	
DB	82	EIQIMHILSEHANVRIEGBTVEYDSTAVHLVMBELCGGELFDRIVQGHYSERQAARLIK	141	
QY	134	ILGVVEACHSLGVHMRDLKPENFLPDSKODAKLKATDFGLSVFYKPGQOYLVDVVGSPYY	193	
DB	142	IVEVVEACHSLGVHMRDLKPENFLPDTIDEDAKLKATDFGLSVFYKPGESFCDDVVGSPYY	201	
QY	194	VAPEVLKCYCFEIDVWSAGVILYILLSGVPPFMAETESGIPRQILOGKLDKFDSPWPPTI	253	
DB	202	VAPEVLRLKLYGPESDVWSAGVILYILLSGVPPFMAESEPGIFRQILLGKLDHFSFEPWSI	261	
QY	254	SEAAKDLIYKMLERSPKRISAEHALCHPWIIVDEQAAADPKLPDPAVLGRLLKQFSQMKIK	313	
DB	262	SDSAKDLIRKMLDQNPKTRLTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAMNKLK	321	
QY	314	KWALRVIAERLSEEBIGGLKELFKMIDTDSNGTITFEE----	369	
DB	322	KWALRVIAERLSEEBIGGLKELFKMIDTDSNGTITFDELKGLKGLKRVGSELMESEIK	381	
QY	370	SLMDAADIDNSGTIDYGEFLAATLHMKNWREBEILVAAFSDFDKDGSYITIDELQSACT	429	
DB	382	DLMDAADIDKSGTIDYGEFIAATVHLNKLEREENLVSAFSYDFDKDGSYITIDELQJACK	441	
QY	430	EFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMWRKGD-GVGRSRPMKNLNFNIADAFGV	488	
DB	442	DFGLDHDHIDDMIKEIDQNDGQIDYGEFAAMWRKNGGIGR-RTMRKTL--NLRDALGL	498	
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KW	hybridisation assay; genetic mapping; gene expression control; promoter;			
KW	termination sequence.			
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PD	06-SEP-2000.			
XX				
PF	25-FEB-2000; 2000EP-0301439.			
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QY 224 PPWAETESGIFRQILQGLKDFKSDPWTISEAAKDLIYKMLERSPKKRISAHEALCHPW 283
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QY 284 IVDEQAAPDKPLDPVLSRLKQFSQMNKIKKMLRVIAERLSEEEIGGLKELFKMIDTDN 343
DB 181 IVDEHAAPDKPLDPVLSRLKQFSQMNKIKKMLRVIAERLSEEEIGGLKELFKMIDTDN 240

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DB 241 SGTITFEELKAGLRVGSSELMSESEIKSLMDAADIDNSGTIDYCEFLAATLHMNKWEREEI 300

QY 404 LVAAFSDFDKDGGYITIDELQSACTEFLGCDTLPDDMIKEIDLNDGKIDFSEFTAMMR 463
DB 301 LVVAFSYFDKGGYITIDELQSACTEFLGCDTLPDDMIKEIDLNDGKIDFSEFTAMMR 360

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AC AAG31158;
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KW Arabidopsis thaliana.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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XX 25-FEB-2000; 2000EP-0301439.
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AC AAG38599;
XX 18-OCT-2000 (first entry)
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
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Query Match 65.7%; Score 1703; DB 21; Length 856;
Best Local Similarity 65.7%; Pred. No. 1.2e-142;
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QY 50 ANYACKSIPKRLVCREDYEDVWREIQIMHLSHPNVVRIKGTVEDSVFVHVMVEVCEG 109
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QY 170 TDFGLSVFVKGOYLVDVVGSPYVAPVLEVKCYGPEIDVNSAGVILYLLSGVPPFWA- 228
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QY 229 -----ETESGIFRQILQGLDFKSDPWPPTISAAXDLIVKMLERSPKKRISAHE 277
Db 588 SEVNLFSMKYTETEQIEQVHLGDLDFSSDPWPSPISAKDLVRKMLVRDPKRRRLTAHQ 647
QY 278 ALCHPWIVDEQAAPDKLPDPAVLSRLKQFSONMKIKKALRVIAERLSEEEIGGLKELFK 337
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QY 398 MEREEILVAFSDFDKSGSVITIDELQSACTEFLGCDTPLDDMIKEIDLNDGKIDFSE 457
Db 768 IEREDHLFAAFSYFDKDESGFITPDELQQAACEEFGVEDARIEEMMRDQDQKGRIDYNE 827
QY 458 FTAMMRKGDGVG 469
Db 828 FVAMMQKGSIMG 839

RESULT 10
AAG38598
ID AAG38598 standard; Protein: 893 AA.
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AC AAG38598;
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DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 47641.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
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Query Match 65.7%; Score 1703; DB 21; Length 1017;

Best Local Similarity 65.7%; Pred. No. 1.5e-142;

Matches 323; Conservative 64; Mismatches 81; Indels 24; Gaps 2;

Qy 2 ETXPNRRP-----SNTVLPYQTPRLRDHYLKKLGGQGFQGTYYLCTEKSTS 49.

Db 509 ETXAEQPKPMHRRVSSAGLRTESVLQRKTENFKFYSLGRKLGGQGFQGTYYLCTEKSTS 568

environmental stress; salinity; drought; temperature; tolerance;
transgenic plant; EST; expressed sequence tag.

Physcomitrella patens.

WO200177356-A2.

18-OCT-2001.

06-APR-2001; 2001WO-US11435.

07-APR-2000; 2000US-196001P.

(BADI) BASF PLANT SCI GMBH.

Da Costa Silva EO, Bohnert HJ, Van Thielens N, Chen R;

Sarria-Millan R;

WPI; 2002-049153/06.

N-PSDB; ABA91081.

New protein, useful for increasing tolerance to environmental stress,
comprises a Protein Kinase Stress-Related Protein selected from
Protein Kinases, Casein Kinase homologs, MAP Kinases or Calcium
dependent protein kinases

Claim 13; Fig 3W; 154pp; English.

Sequences AAM52830-AAM52842 represent novel protein kinase stress-related
proteins (PKSRPs) from the moss *Physcomitrella patens*, and sequences
ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA
sequences were obtained from expressed sequence tags (ESTs; ABA91056-
ABA91068) derived from *Physcomitrella patens* cDNA libraries. The PKSRPs
of the invention comprise protein kinase-6 (PK-6), protein kinase-7
(PK-7), protein kinase-8 (PK-8), protein kinase-9 (PK-9), casein kinase
homologue-1 (CK-1), casein kinase homologue-2 (CK-2), casein kinase
homologue-3 (CK-3), mitogen-activated protein (MAP) kinase-2 (MPK-2),
MAP kinase-3 (MPK-3), MAP kinase-4 (MPK-4), MAP kinase-5 (MPK-5),
calcium-dependent protein kinase-1 (CPK-1), and calcium-dependent protein
kinase-2 (CPK-2). When overexpressed, the PKSRPs are able to confer
tolerance to environmental stresses such as salinity, drought,
temperature, metal, chemical, pathogenic and oxidative stress.
Physcomitrella patens PKSRP nucleic acids may be used to generate
transgenic plants and seeds with increased tolerance to salinity, drought
and temperature. The transgenic plants generated can be monocots or
dicots and are especially maize, wheat, rye, oat, triticale, rice,
barley, cotton, rapeseed, cassava, sunflower, tagetes, leguminous plants
(e.g., soybean, peanut, *Vicia species*, alfalfa), solanaceous plants
(e.g., potato, tobacco, aubergine, pepper, tomato), coffee, cacao, tea,
Salix species, oil palm, coconut, perennial grasses and forage crops. The
PKSRP nucleotide and proteins may also be used in evolutionary and
protein structural studies and as markers for specific regions of
the genome.

Sequence 549 AA;

Query Match 58.2%; Score 1509.5; DB 23; Length 549;

Best Local Similarity 60.8%; Pred. No. 1.1e-125;

Matches 290; Conservative 70; Mismatches 112; Indels 5; Gaps 3;

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QY 62 LVCREDEYVREIQIMHLLSEHPVVRVIRKGTVEDSVFVHVMVECGEGGELFDRIVSKGH 121
Db 129 LTKSKEDIEDKREVMQHLSGTFNIVLWKDVEDKSHVHVLNLCAGGELFDRITAKGH 188
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Db 189 YSRAAADMCRIWVNVHRSGLGVFHRDLKPENFLLASKAEDAPLKATDFGLSTPFKPG 248
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QY 242 KLDPKSDPWTITSEAAKDLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKPLDPAVLS 301
Db 309 HIDFENDPWPKISNGAKDLVRKMLNPVKIRLTAQQVLNHPMKEDGDAEDVPLDNAVL 368
QY 302 RLKQFSQMNKIKKWLNRVIAERLSEEEIGGLKELFKMIDTNSCTITFEELKAGLKRVS 361
Db 369 RLKNFSAANKMKKALKLVIAESLSEEEIVGLREMFKSIDTNSGTVTTFEELKEGLKOGS 428
QY 362 ELMESEIKSLMDAADIDNSGTIDYGEPLAATLHMKNKMEREEILVAASFDFDKDGSVITI 421
Db 429 KLNESDIRKLMEAADVDGNGKIDNFENFISATMNMNTEKEDHLWAAEFHEDTNSGVITI 488
QY 422 DELQSACTEFLGCD-TPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
Db 489 DELQEAEMKNGMGDPETIQEIISEVDTNDGRIDYDEFVAMMRKNGPANGGTVNK 545

RESULT 14

AAG31159

ID AAG31159 standard; Protein; 408 AA.

AC AAG31159;

XX 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 37373.

XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

XX Arabidopsis thaliana.

XX EF1033405-A2.

PN 06-SEP-2000.

PD 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 21-MAR-1999; 99US-0125788.

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PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.

[illegible]

Search completed: November 28, 2003, 10:35:30
Job time : 83 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 10:31:21 ; Search time 43 Seconds
(without alignments)
1107.058 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593
Sequence: 1 METKPNRRPSNTVLPYQTP.....KNLNFNIADAFGVGDKSD 495

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	2593	100.0	495	S46284	calcium-dependent
2	2458	94.8	501	G85097	hypothetical prote
3	2030	78.3	490	T08873	calcium-dependent
4	1944	75.0	508	A43713	calcium-dependent
5	1847.5	71.2	490	S71776	calcium-dependent
6	1752	67.6	492	T03271	calcium-dependent
7	1751	67.5	487	S71770	calcium-dependent
8	1745	67.3	554	T03263	calcium-dependent
9	1742	67.2	556	T06126	calcium-dependent
10	1731	66.8	544	D84550	calcium-dependent
11	1724	66.5	610	A45082	probable calmoduli
12	1709.5	65.9	573	T029940	calcium-dependent
13	1700.5	65.6	484	T05650	calcium-dependent
14	1672.5	64.5	639	T02784	calcium-dependent
15	1640.5	63.3	583	H84810	calcium-dependent
16	1630	62.9	451	S56717	probable calcium-d
17	1586	61.2	542	S56651	calcium-dependent
18	1484.5	57.3	540	T01989	calcium-dependent
19	1482	57.2	531	D85059	calcium-dependent
20	1482	57.2	533	S56652	probable calcium d
21	1480	57.1	531	T02993	calcium-dependent
22	1463.5	56.4	521	G94543	calcium-dependent
23	1462	56.4	529	S71774	calcium-dependent
24	1460.5	56.3	513	T02259	calcium-dependent
25	1460	56.3	534	JC1515	calcium-dependent
26	1458.5	56.2	538	T08874	calcium-dependent
27	1449	55.9	554	T05476	calcium-dependent
28	1437.5	55.4	465	T03024	calcium-dependent
29	1432.5	55.2	532	T14335	protein kinase, ca

30	1431	55.2	514	2	T10938	calcium-dependent
31	1381	53.3	545	2	H86322	calcium-dependent
32	1367.5	52.7	493	1	S46283	calcium-dependent
33	1363	52.6	541	2	F96776	hypothetical prote
34	1361	52.5	553	1	T02139	calcium-dependent
35	1356.5	52.3	520	2	F85059	probable calcium d
36	1325.5	51.1	560	2	T46189	calcium-dependent
37	1324.5	51.1	425	2	S17759	protein kinase, ca
38	1313.5	50.7	533	1	S71778	calcium-dependent
39	1287.5	49.7	520	2	C84774	probable calcium-d
40	1280.5	49.4	530	2	A84847	probable Ca2+ depe
41	1238.5	47.8	582	2	E84721	probable calcium-d
42	1229.5	47.4	575	2	C85059	probable calcium d
43	1225.5	47.3	503	2	T51156	calcium dependent
44	1176.5	45.4	591	2	S54788	calcium-stimulated
45	1056.5	40.7	571	2	T00835	calcium-dependent

ALIGNMENTS

RESULT 1

S46284

calcium-dependent protein kinase (EC 2.7.1.-) 2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Jun-2000

C:Accession: S46284

R:Urao, T.; Katagiri, T.; Mizoguchi, T.; Yamaguchi-Shinozaki, K.; Hayashida, N.; Shino;

Mol. Gen. Genet. 244, 331-340, 1994

A:Title: Two genes that encode Ca(2+)-dependent protein kinases are induced by drought

A:Reference number: S46283; MUID:94359455; PMID:8078458

A:Accession: S46284

A:Molecule type: mRNA

A:Residues: 1-495 <URA>

A:Cross-references: EMBL:D21806; NID:gi235717; PIDN:BAA04830.1; PID:g604881

C:Gene: CDPK2

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein k;

C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specif;

F:24-284/Domain: protein kinase homology <Kin>

F:32-40/Region: protein kinase ATP-binding motif

F:327-359/Domain: calmodulin repeat homology <EF1>

F:363-395/Domain: calmodulin repeat homology <EF2>

F:399-431/Domain: calmodulin repeat homology <EF3>

F:433-465/Domain: calmodulin repeat homology <EF4>

F:55/Active site: Lys #status predicted

Query Match 100.0%; Score 2593; DB 1; Length 495;
Best Local Similarity 100.0%; Pred. No. 1.7e-89;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	METKPNRRPSNTVLPYQTPRLRDHYLLGKLGQGGFGTTLCTEKSTSANVACKSI	PKR 60
Db	1	METKPNRRPSNTVLPYQTPRLRDHYLLGKLGQGGFGTTLCTEKSTSANVACKSI	PKR 60
Qy	61	KLVCREDYEDVWREIQIMHLSHNNVRIKCTYEDSVFVHVMVECEGELFDRIV	SKG 120
Db	61	KLVCREDYEDVWREIQIMHLSHNNVRIKCTYEDSVFVHVMVECEGELFDRIV	SKG 120
Qy	121	HFSEAEAVKLIKTLGWAEACHSLGVMDLKPENFLDPSKDDAKLKATDFGLSV	FYKFP 180
Db	121	HFSEAEAVKLIKTLGWAEACHSLGVMDLKPENFLDPSKDDAKLKATDFGLSV	FYKFP 180
Qy	181	GOYLDVGVSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIF	RQILQ 240
Db	181	GOYLDVGVSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIF	RQILQ 240
Qy	241	GKLDKSPWPMTTISEAAKDLIYKMLERSPKKISAEALCHPWIVDEQAAPK	PLDPAVL 300
Db	241	GKLDKSPWPMTTISEAAKDLIYKMLERSPKKISAEALCHPWIVDEQAAPK	PLDPAVL 300
Qy	301	SRLKQFSQMNKIKQALRVIAERLSEETGGIKELFKMIDTNSGTITFEELK	KAGLKRVG 360

Db 301 SRLKQFSQMNKIKKXALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVG 360
Qy 361 SELMESEIKSLMDAADINSCTIDYGEFLAATLHNKMKEREELVAAFSDFDKDGSYGIT 420
Db 361 SELMESEIKSLMDAADINSCTIDYGEFLAATLHNKMKEREELVAAFSDFDKDGSYGIT 420
Qy 421 IDELOQACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNF 480
Db 421 IDELOQACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNF 480
Qy 481 NIADAFGVGDGKSD 495
Db 481 NIADAFGVGDGKSD 495

RESULT 2
G85097
hypothetical protein AT4g09570 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 23-Mar-2001
C:Accession: G85097
R:ano:ymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083486; PMID:10617198
A:Accession: G85097
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-501 <STO>
A:Cross-references: GB:NC_001268; NID:g7267652; PIDN:CAB78080.1; GSPDB:GN00140
C:Genetics:
A:Gene: At4g09570
A:Map position: 4
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C:Keywords: EF hand

Query Match 94.8%; Score 2458; DB 2; Length 501;
Best Local Similarity 94.8%; Pred. No. 1.7e-84;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;
Qy 4 KPNRPRESNLPVQTPRLRDHYLLGKLGQGGQGTLYLCTEKSTSNANYACKSIPKRLV 63
Db 3 KPNRPRESNLPVETPRLDHYLLGKLGQGGQGTLYLCTEKSSSNANYACKSIPKRLV 62
Qy 64 CRDIEDVWREIQIMHLSHPNVRIKGTYESVVFHIVMEVCEGGEFLDRIVSKGHFS 123
Db 63 CRDIEDVWREIQIMHLSHPNVRIKGTYESVVFHIVMEVCEGGEFLDRIVSKGCF 122
Qy 124 ERAVKLIKTLGVVEACHSLGVMHRDLKPEFLFDSPKDDAKLKATDFGLSVFYKPGQY 183
Db 123 ERAVKLIKTLGVVEACHSLGVMHRDLKPEFLFDSPKDDAKLKATDFGLSVFYKPGQY 182
Qy 184 LYDVGSPYVVAPEVLKCKYGPIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLK 243
Db 183 LYDVGSPYVVAPEVLKCKYGPIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLK 242
Qy 244 DFKSDPWTITSEAAKOLIIYKMLERSPKRISAEALCHPMIVDEQAAPKPLDPVLSRL 303
Db 243 DFKSDPWTITSEGAOLIIYKMLDRSPKRISEAELCHPMIVDEHAAPKPLDPVLSRL 302
Qy 304 KQFSQMNKIKKALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSEL 363
Db 303 KQFSQMNKIKKALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSEL 362
Qy 364 MSEIKSLMDAADINSCTIDYGEFLAATLHNKMKEREELVAAFSDFDKDGSYGITIDE 423
Db 363 MSEIKSLMDAADINSCTIDYGEFLAATLHNKMKEREELVAAFSDFDKDGSYGITIDE 422
Qy 424 LQACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNFIA 483
Db 423 LQACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNFIA 482
Qy 484 DAFGVGDG----BKSD 495

Db 483 EAFGVEDTSSTAKSD 498
RESULT 3
T08873
calcium-dependent protein kinase (EC 2.7.1.1-) beta - soybean
C:Species: Glycine max (soybean)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jan-2000
C:Accession: T08873
R:Lee, J.Y.; Yoo, B.C.; Harmon, A.C.
submitted to the EMBL Data Library, September 1996
A:Reference number: Z16505
A:Accession: T08873
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-490 <LEE>
A:Cross-references: EMBL:U69173; NID:g2501763; PID:g2501764
C:Genetics:
A:Gene: CDPK beta
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein k
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specif
F:22-282/Domain: protein kinase homology <KIN>
F:30-38/Region: protein kinase ATP-binding motif
F:324-356/Domain: calmodulin repeat homology <EFH>
F:53/Active site: Lys #status predicted
Query Match 78.3%; Score 2030; DB 2; Length 490;
Best Local Similarity 81.3%; Pred. No. 1.1e-68;
Matches 386; Conservative 43; Mismatches 45; Indels 2; Gaps 2;
Qy 14 VLPVQTPRLRDHYLLGKLGQGGQGTLYLCTEKSTSNANYACKSIPKRLVCREDYEDVWR 73
Db 12 VLPVQTPARLADHYLLGKLGQGGQGTLYLCTHKVTGKLYACKSIPKRLKQCQEDYDDVWR 71
Qy 74 EIQIMHLSHPNVRIKGTYESVVFHIVMEVCEGGEFLDRIVSKGHFSEREAVKLK 133
Db 72 EIQIMHLSHPNVQIQGTYESVVFHIVMEVCEGGEFLDRIVSKGHFSEREAAKLK 131
Qy 134 ILGVVEACHSLGVMHRDLKPEFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPY 193
Db 132 ILGVVEACHSLGVMHRDLKPEFLFDPGDAQMKATDFGLSVILQARQAFHDVVGSPY 191
Qy 194 VAPEVLKCKYGPIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWTI 253
Db 192 VAPEVLCKYGPIDVMSAGVILYLLSGVPPFWAETESGIFRQILNGDDLFVSEPPSI 251
Qy 254 SEAAKOLIIYKMLERSPKRISAEALCHPMIVDEQAAPKPLDPVLSRLKQFSQMNKIK 313
Db 252 SENAKELVKQLDRDPKRISEAHEVLCNPWVDD--IAPDKPLDSAVLTRLKHFSAMNKLK 310
Qy 314 KVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSELMESEIKSLMD 373
Db 311 KVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKEGLKSVGNSLMESEIKSLME 370
Qy 374 AADIDNSGTTIDYGEFLAATLHNKMKEREELVAAFSDFDKDGSYGITIDELOQACTEFLG 433
Db 371 AADIDNNGSIDYGEFLAATLHNKMKEREELVAAFSDFDKDGSYGITIDELOQACDQFSL 430
Qy 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD--GVGRSRTMMKNLNFNIADAFV 488
Db 431 GDVHLDKMIKEIQDNDGRIDYAEFAAMMKGGDPNMGRSRTWKGNLNFNIADAFGM 486

RESULT 4
A43713
calcium-dependent protein kinase (EC 2.7.1.1-) - soybean
C:Species: Glycine max (soybean)
C:Date: 03-Mar-1993 #sequence_revision 14-Jul-1994 #text_change 11-Jun-1999
C:Accession: A43713
R:Harper J.F.; Suesman, M.R.; Schaller, G.E.; Putnam-Evans, C.; Charbonneau, H.; Harm
Science 252, 951-954, 1991
A:Title: A calcium-dependent protein kinase with a regulatory domain similar to calmod

submitted to the EMBL Data Library, February 1995

A;Description: Expression of the calcium-dependent protein kinase gene family in Arabid

A;Reference number: S71197

A;Accession: S71902

A;Molecule type: DNA

A;Residues: 1-164,'S',166-239,'E',241-300,'KF',303-350,'S',352-490 <HOW>

A;Cross-references: EMBL:U20626; NID:g836945; PIDN:AAA67657.1; PID:g836946

R;Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N.

submitted to the EMBL Data Library, January 1995

A;Description: Expression of the calcium dependent protein kinase gene family in Arabid

A;Reference number: S71196

A;Accession: S71196

A;Molecule type: mRNA

A;Residues: 1-164,'S',166-239,'E',241-300,'KF',303-350,'S',352-490 <HOA>

A;Cross-references: EMBL:U20388; NID:g836937; PIDN:AAA67653.1; PID:g836938

C;Genetics:

A;Gene: CDPK9

A;Introns: 177/1; 225/1; 276/1; 370/3; 445/3

C;Superfamily: calcium-dependent protein kinase

C;Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific

F;20-280/Domain: protein kinase homology <KIN>

F;28-36/Region: protein kinase ATP-binding motif

F;323-355/Domain: calmodulin repeat homology <EF1>

F;359-391/Domain: calmodulin repeat homology <EF2>

F;395-427/Domain: calmodulin repeat homology <EF3>

F;429-461/Domain: calmodulin repeat homology <EF4>

F;51/Active site: Lys #status predicted

Query Match 71.2%; Score 1847.5; DB 1; Length 490;

Best Local Similarity 73.5%; Pred. No. 5.8e-62;

Matches 355; Conservative 52; Mismatches 69; Indels 7; Gaps 2;

QY 1 METKPNRPSPNTLVLPYQTPRLRDHYLLGCKLGQGGTGYTLCTEKSTSNANYACKSIPKR 60

Db 1 MANKPTR-----WLPYKTNQVEDNIFLGQVLGGQGGTFLCTHKTQTKGKLACKSIPKR 56

QY 61 KLVCREDDYEDVMREIQIMHHLSEHPNVVRIKGTYESVFPVHIVMEYCEGGEFLDRIIVSKG 120

Db 57 KLLCQEDYDDVLRREIQIMHHLSEYPNVRIESAYEDTKNVHLVMEICEGGEFLDRIIVKRG 116

QY 121 HFSEREAVKLIKTILGVWEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKP 180

Db 117 HYSEREAALKIKTIQVWEACHSLGVVHRDLKPNFLFSSDEDAKLKATDFGLSVFCTP 176

QY 181 GOVLYDVGSPYYVAPEVLKCYGEIDVWSAGVILYLLSGVPPPPWAETESGIFRQILQ 240

Db 177 GFAFSELVGSAYVAPEVLKHYGPECVWSAGVILYLLCGFPFPFPAESETGIFRKILQ 236

QY 241 GKLDKFSDPWPTTISEAAKDLIYKMLERSPKKRIISAHEALCPWIVDEQAAPDKLPDPAVL 300

Db 237 GKLDPEINPWSIPSESADKLIKMLSPKRLTAHOVLCHPWIVDDKVAPDKPLDCAVV 296

QY 301 SRLKQFSQNNKIKKQALRVIAERLSEETGGKLELFKMDITDTONSGTITFEELKAGLKRYG 360

Db 297 SRLKQGSAMNKKQALRVIAERLSEETGGKLELFKMDITDKSGTITFEELKQGMRRVG 356

QY 361 SELMESEITKSLMDADINDSGTIDYGEFLAATLHNKQKEREILVAAFSDFDKDSGYIT 420

Db 357 SELMESEITQELLRAADVDPSGTIDYGEFLAATLHNKLEREENLVAAFSFFDKDASGYIT 416

QY 421 IDELOSACTEFLGCTPLDDMIKEIDLNDKIDFSEFTAMMKRGDGVGRS---RTMKKN 477

Db 417 IEELQANKEFGINDSNDEMIKDQNDQGDQIDYGEFVAMMKRKGNGTGGGIRGRTRMNS 476

QY 478 LNF 480

Db 477 LNF 479

RESULT 6

T03271

C;Species: Zea mays (maize)

calcium-dependent protein kinase (EC 2.7.1.-) 1 - maize

C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Jun-2000
C;Accession: T03271
R;Berberich, T.; Kusano, T.
Mol. Gen. Genet. 254, 275-283, 1996
A;Title: Cycloheximide induces a subset of low temperature-inducible genes in maize.
A;Reference number: Z14873
A;Accession: T03271
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-492 <BER>
A;Cross-references: EMBL:D84408; PIDN:BAA12338.1
A;Experimental source: strain honey bantum
A;Note: low temperature-inducible
C;Genetics:
A;Gene: CDPK1
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase
C;Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
F;25-285/Domain: protein kinase homology <KIN>
F;33-41/Region: protein kinase ATP-binding motif
F;328-360/Domain: calmodulin repeat homology <EF1>
F;364-396/Domain: calmodulin repeat homology <EF2>
F;400-432/Domain: calmodulin repeat homology <EF3>
F;434-466/Domain: calmodulin repeat homology <EF4>
F;56/Active site: Lys #status predicted
Query Match 67.6%; Score 1752; DB 1; Length 492;
Best Local Similarity 70.8%; Pred. No. 2e-58;
Matches 334; Conservative 54; Mismatches 83; Indels 2; Gaps 2;
QY 13 TVLPYQTPRLRDHYLLGKLGQGGFGTTTCTKSTSANVACKSIKPKLVCREDEYDW 72
DB 14 SVLGHTTPNLDYALGRKLGQGGFGTTTCTELATGIDYACKSIKPKLVCREDEYDW 73
QY 73 REIQMHHLSEHPNVRIKGYEDSVFVHIVMEVCEGGELFDRIIVSKGHFSERAVKLK 132
DB 74 REIQMHHLSEHPNVRIKGYEDSVFVHIVMEVCEGGELFDRIIVSKGHFSERAVKLK 133
QY 133 TILGVVEACHSLGVHMDLKPENFLDPSKDDAKLKATDFGLSVFYPKQGYLYDVVGSY 192
DB 134 IIVGVVEACHSLGVHMDLKPENFLNANRDDLKSLKAIDFGLSVFYPKQGYLYDVVGSY 193
QY 193 YVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWP 252
DB 194 YVAPEVLKCYGPAADVMTAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWP 253
QY 253 ISEAAKDLIYKMLERPKRISAEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQMNKI 312
DB 254 ISDSAKDLIRRLNRPAPERLTAHEVLCHPWIRHGVAPDRPLDPAVLRLKQFSQMNKI 313
QY 313 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKRKVGSELMESEIKSLM 372
DB 314 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKRKVGSELMESEIKSLM 373
QY 373 DAADINSGTIDYGFELAAATLHNMKVEREILVAAFSDFDKGSGYITIDELQSACTERG 432
DB 374 DAADINSGTIDYGFELAAATLHNMKVEREILVAAFSDFDKGSGYITIDELQSACTERG 433
QY 433 LCDTPLDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMKNLNFNIAD 484
DB 434 MPDAFLDDVINEADQNDGRIDYGBFVAMTKGNMGVGR-RTMRNSLNLSMRD 485
RESULT 7
S71770
calcium-dependent protein kinase (EC 2.7.1.-) - mung bean
C;Species: Vigna radiata (mung bean)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-Jun-1999
C;Accession: S71770
R;Botella, J.R.; Arteca, J.M.; Somodevilla, M.; Arteca, R.N.
Plant Mol. Biol. 30, 1129-1137, 1996
A;Title: Calcium-dependent protein kinase gene expression in response to physical and ch
A;Reference number: S71770; MUID:96311003; PMID:8704124
A;Accession: S71770

A;Molecule type: mRNA
A;Residues: 1-487 <BOT>
A;Cross-references: EMBL:U08140; NID:9667124; PIDN:ABC49405.1; PID:9967125
A;Experimental source: strain Rwlcz, cv. Berken, clone pvr-CDPK-1
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein ki
C;Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specifi
F;22-282/Domain: protein kinase homology <KIN>
F;30-38/Region: protein kinase ATP-binding motif
F;325-357/Domain: calmodulin repeat homology <EF2>
F;361-393/Domain: calmodulin repeat homology <EF3>
F;397-429/Domain: calmodulin repeat homology <EF4>
F;431-463/Domain: calmodulin repeat homology <EF5>
F;53/Active site: Lys #status predicted
Query Match 67.5%; Score 1751; DB 1; Length 487;
Best Local Similarity 69.1%; Pred. No. 2.1e-58;
Matches 327; Conservative 64; Mismatches 80; Indels 2; Gaps 2;
QY 14 VLPYQTPRLRDHYLLGKLGQGGFGTTTCTKSTSANVACKSIKPKLVCREDEYDW 73
DB 12 VLGHKTPNIRDLYTLGRKLGQGGFGTTTCTENSTSNVACKSIKPKLVCREDEYDW 71
QY 74 EIQIMHHLSEHPNVRIKGYEDSVFVHIVMEVCEGGELFDRIIVSKGHFSERAVKLK 133
DB 72 EIQIMHHLSEHPNVRIKGYEDSVFVHIVMEVCEGGELFDRIIVSKGHFSERAVKLK 131
QY 134 IILGVVEACHSLGVHMDLKPENFLDPSKDDAKLKATDFGLSVFYPKQGYLYDVVGSY 193
DB 132 IIVGVVEACHSLGVHMDLKPENFLNANRDDLKSLKAIDFGLSVFYPKQGYLYDVVGSY 191
QY 194 YVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWP 253
DB 192 YVAPEVLKCYGPAADVMTAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWP 251
QY 254 SEAAKDLIYKMLERPKRISAEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQMNKI 313
DB 252 SUSGKDLIRRLNRPAPERLTAHEVLCHPWIRHGVAPDRPLDPAVLRLKQFSQMNKI 311
QY 314 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKRKVGSELMESEIKSLM 373
DB 312 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKRKVGSELMESEIKSLM 371
QY 374 DAADINSGTIDYGFELAAATLHNMKVEREILVAAFSDFDKGSGYITIDELQSACTERG 433
DB 372 AADVDKSGTIDYGFELAAATLHNMKVEREILVAAFSDFDKGSGYITIDELQSACTERG 431
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMKNLNFNIAD 485
DB 432 TDAFLDDVINEADQNDGRIDYGBFVAMTKGNMGVGR-RTMRNSLNLSMRD 483
RESULT 8
T03263
calcium-dependent protein kinase (EC 2.7.1.-) 7 - maize
C;Species: Zea mays (maize)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T03263
R;Saijo, Y.; Hata, S.; Sheen, J.; Izui, K.
Biochim. Biophys. Acta 1350, 109-114, 1997
A;Title: CDNA cloning and prokaryotic expression of a maize calcium-dependent protein
A;Reference number: Z14815; MUID:97201047; PMID:9048876
A;Accession: T03263
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-554 <SAI>
A;Cross-references: EMBL:D87042; NID:91504051; PIDN:BAA13232.1; PID:91504052
A;Experimental source: strain inbred line H84, clone CDPK7
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein ki
C;Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specifi
F;89-349/Domain: protein kinase homology <KIN>
F;97-105/Region: protein kinase ATP-binding motif
F;392-424/Domain: calmodulin repeat homology <EF1>
F;428-460/Domain: calmodulin repeat homology <EF2>

6 NRRPSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTVLTCTEKSTSANACKSIPKRKLVC 65

QY	126	EAVKLIK	TILGVE	ACHSLG	VNHRDL	KPENFL	FDSPKDD	AKLKAT	DFGLSV	FYFKPGQ	LYL	185
----	-----	---------	--------	--------	--------	--------	---------	--------	--------	---------	-----	-----

Db 185 KAAELTKIIVGVVEACHSLGVMHRLDKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQIFK 244
QY 186 DVVGSPPYVAPEVLKCCYGPEDVWSAGVILYILLSGVPPFPWFAETSGIFRQILQGLKDF 245
Db 245 DVVGSPPYVAPEVLKCCYGPEDVWSAGVILYILLSGVPPFPWFAETSGIFRQILQGLKDF 304
QY 246 KSDPWPPTSBAKDLIYKMLERSPKGRISAHEALCHPWIDQOAPDKPLDPAVLSRLKQ 305
Db 305 DTPDPWPVSDSAKDLIRKMLCSPSERLTAHEVLRHWPICENGVAPOALDPAVLSRLKQ 364
QY 306 FSQWNKKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTTIFEEELKAGLKRVSGLME 365
Db 365 FSQWNKKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTTIFEEELKAGLKRVSGLME 424
QY 366 SEIKSLMDAADIDNSGTTIDYGEFLAATLHNMKMERERILVAATSDPKDGSYTTIDELQ 425
Db 425 TEIRDLMEADVNSGTTIDYSEFIATLHNLKLEREHLVSAFOYDFKDGSGYTTIDELQ 484
QY 426 SACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-VGGRSRTVMKMLNFNIAD 484
Db 485 QSCIEHGMTDFLEDDIIEVDNDGNDGRIDYEEFVAMQKGNAGVGR-RTMKNSLINSMRD 543
RESULT 11
A49082
calcium-dependent protein kinase (EC 2.7.1.-) AK1 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-Jun-1999
C:Accession: A49082
R:Harper, J.F.; Binder, B.M.; Suesman, M.R.
Biochemistry 32, 3282-3290, 1993
A:Title: Calcium and lipid regulation of an Arabidopsis protein kinase expressed in Esch
A:Reference number: A49082; MUID:93213795; PMID:7916621
A:Contents: ecotype Columbia
A:Accession: A49082
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-610 <HAR>
A:Cross-references: GB:14771; NID:G289189; PIDN:AAA32761.1; PID:G304105
A:Note: sequence extracted from NCBI backbone (NCBIN:128903, NCBIPI:128904)
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
F:148-408/Domain: protein kinase homology <KIN>
F:156-164/Region: protein kinase ATP-binding motif
F:451-483/Domain: calmodulin repeat homology <EF1>
F:487-519/Domain: calmodulin repeat homology <EF2>
F:523-555/Domain: calmodulin repeat homology <EF3>
F:557-589/Domain: calmodulin repeat homology <EF4>
F:179/Active site: Lys #status Predicted

QY 282 PWIVDEQAPDKPLDPAVLSRLKOFQSMNKIKKMLARVIAERLSEEEIGGLKELFKMIDT 341
Db 406 PWVQVGVADPKPLDPAVLSRLKOFQSMNKIKKMLARVIAERLSEEEIGGLKELFKMIDT 465
QY 342 DMSGTTTFEELKAGLKRVSSELSEIKSLMDAADIDNSGTTIDYGEFLAATLHNMKMER 401
Db 466 DKSGQITFEELKAGLKRVSSELSEIKSLMDAADIDNSGTTIDYGEFLAATLHNMKMER 525
QY 402 EILVAAPSPDKDGSYTTIDELQSACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAM 461
Db 526 DHLFAAFTYFDKDGSGYTTIDELQSACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAM 585
QY 462 MRKGDGVGRSRTVMKMLNFNIA 483
Db 586 MQKGSITGGPVKMGLEKSFSA 607
RESULT 12
T09940
calcium-dependent protein kinase (EC 2.7.1.-) CDPK - pumpkin
N:Alternate names: calcium-dependent calmodulin-independent protein kinase CDPK
C:Species: Cucurbita pepo (pumpkin)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09940
R:Ellard-Ivey, M.; Hopkins, R.B.; White, T.J.; Lomax, T.L.
Plant Mol. Biol. 39, 199-208, 1999
A:Title: Cloning, expression and N-terminal myristoylation of CpCPK1, a calcium-depend
A:Reference number: Z16898; MUID:99178773; PMID:10080688
A:Accession: T09940
A:Molecule type: mRNA
A:Residues: 1-573 <ELL>
A:Cross-references: EMBL:U90262; NID:G1899174; PIDN:AAB49984.1; PID:G1899175
A:Experimental source: etiolated hypocotyls
C:Genetics:
C:Gene: CPK1
C:Function:
A:Description: serine/threonine-specific protein kinase activated by direct binding of
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein k
C:Keywords: ATP; calcium binding; EF hand; membrane protein; myristylation; phosphotri
F:108-368/Domain: protein kinase homology <KIN>
F:447-479/Domain: calmodulin repeat homology <EFH>

Query Match 66.5%; Score 1724; DB 1; Length 610;
Best Local Similarity 65.5%; Pred. No. 2.5e-57;
Matches 329; Conservative 62; Mismatches 91; Indels 20; Gaps 2;
QY 2 ETKP-----NPRP-----SNTVLPTQTRLDHYLLGKLGQGGQGTYY 41
Db 106 ETKPSKPPPAKPKPKMKRVSSAGLATESVLQRTNFKEFSLGRLKLGQGGQGTTF 165
QY 42 LCTEKSTANSYACKSIPKRLKVCREDYEDVWREIQIMHLSHPNVIRIKGTYESVVFH 101
Db 166 LCVEKTTGKEFACKSIKRLTDEVEDVREIQIMHLSHPNVIRIKGTYESVVFH 225
QY 102 IYMEVCEGELFDRIVSKGHFSEREAVALIKITILGVVEACHSLGVMHRLDKPENFLFOSP 161
Db 226 LVMECCAGGELFDRIVSKGHFSEREAVALIKITILGVVEACHSLGVMHRLDKPENFLFOSP 285
QY 162 KDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLKCCYGPEDVWSAGVILYILL 221
Db 286 HEDSLKLTIDFGLSNFFKPPDDVFTDVVGSPPYVAPEVLKCCYGPEDVWSAGVILYILL 345
QY 222 GVPFWAETESGIFRQILQGLKDFKSDPWPPTSBAKDLIYKMLERSPKGRISAHEALCH 281
Db 346 GVPFWAETESGIFRQILQGLKDFKSDPWPPTSBAKDLIYKMLERSPKGRISAHEALCH 405

Query Match 65.9%; Score 1709.5; DB 2; Length 573;
Best Local Similarity 64.8%; Pred. No. 8.3e-57;
Matches 321; Conservative 78; Mismatches 79; Indels 17; Gaps 3;
QY 4 KPNRP-----RP-----SNTVLPTQTRLDHYLLGKLGQGGQGTYYLCTEKS 47
Db 72 KPEPPMEKVRPVMKRVSGAGLGGSVLQTKTGNFKEYYSLLGKLGQGGQGTYYMCVEKA 131
QY 48 TSANYACKSIPKRLKVCREDYEDVWREIQIMHLSHPNVIRIKGTYESVVFHIMEYC 107
Db 132 TGKEYACKSIKRLKVCREDYEDVWREIQIMHLSHPNVIRIKGTYESVVFHIMEYC 191
QY 108 EGELFDRIVSKGHFSEREAVALIKITILGVVEACHSLGVMHRLDKPENFLFVSKEESL 167
Db 192 AGGELFDRIVSKGHFSEREAVALIKITILGVVEACHSLGVMHRLDKPENFLFVSKEESL 251
QY 168 KATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLKCCYGPEDVWSAGVILYILLSGVPPFW 227
Db 252 KTDIFGLSMFFKPGKFNDDVVGSPYVAPEVLKCCYGPEDVWSAGVILYILLSGVPPFW 311
QY 228 AETESGIFRQILQGLKDFKSDPWPPTSBAKDLIYKMLERSPKGRISAHEALCHPWIDE 287
Db 312 AESSEGIFEEVHLHGLDFFSSDPWPSISDSAKDLVRRMLVRDPKRLTAYEVLCHPWQVD 371
QY 288 QAAPDKPLDPAVLSRLKOFQSMNKIKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTI 347
Db 372 GVADPKPLDPAVLSRLKOFQSMNKIKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTI 431
QY 348 TFEELKAGLKRVSSELSEIKSLMDAADIDNSGTTIDYGEFLAATLHNMKMEREILVAA 407

Db 432 TFEELKAGLKKFGANLKESEIYDLMOAADINDNGTTIDYGEFVAATLHLNKEIEKEDLLAA 491
QY 408 FSDFOKDGSGYITIDELQACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDG 467
Db 492 FSYFDKDGSGFITHDELQACKFGLIEDLOMBEMREVDQNDGSDYNEFVAMQKGVN 551
QY 468 VGRSRTMMKNLNFNI 482
Db 552 VNTGKKGLQS-SFSI 565

RESULT 13
T05650
calcium-dependent protein kinase (EC 2.7.1.1-) F20D10.350 - Arabidopsis thaliana
N:Alternate names: protein F20D10.350
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000
C:Accession: T05650
R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, February 1999
A:Reference number: Z15420
A:Accession: T05650
A:Molecule type: DNA
A:Residues: 1-484 <BEV>
A:Cross-references: EMBL:AL035538
A:Experimental source: cultivar Columbia; BAC clone F20D10
C:Genetics:
A:Map position: 4
A:Introns: 179/1; 227/1; 278/1; 316/3; 372/3; 447/3
A:Note: F20D10.350
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific
F:22-282/Domain: protein kinase homology <KIN>
F:30-38/Region: protein kinase ATP-binding motif
F:325-357/Domain: calmodulin repeat homology <EF1>
F:361-393/Domain: calmodulin repeat homology <EF2>
F:397-429/Domain: calmodulin repeat homology <EF3>
F:431-463/Domain: calmodulin repeat homology <EF4>
F:53/Active site: Lys #status predicted

Query Match 65.6%; Score 1700.5; DB 2; Length 484;
Best Local Similarity 69.3%; Pred. No. 1.5e-56;
Matches 325; Conservative 60; Mismatches 81; Indels 3; Gaps 2;
QY 14 VLPYQTPRLRDHYLLGKLGQOGQGTTLCTEKSATSANYACKSIPKRLKVCREDYEDVVR 73
Db 12 VLQKQTPSIDRLYSGLHKLGGQGFQGTVMCKEISTGREYACKSITKRLKISKEDVEDVRR 71
QY 74 EIQIMHLSHEHPNVVRIKGTYESDVVHVMVECEGGLFDRIVSKGHPSEREAVKLTKT 133
Db 72 EIQIMHLLAGYKNVITIKGAYEDPDLVYHVMELCSGGLFDRIIQORHYSEKAAELIKI 131
QY 134 ILGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFVKPGQYLDVVGSPVY 193
Db 132 IVGVVEACHSLGVNHRDLKPNFLVKNDDPSLKAIDFGLSVFPKPGQIFEDVVGSPVY 191
QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILOGKLDFKSPWPPTI 253
Db 192 VAPEVLLKHGPEADVWTAGVILYILVSGVPPFWAETQGGIFDAVLKGHIDFSDPWPILI 251
QY 254 SEAAKDLIYKMLERSPKRISAEALCHPWIVDEQAADPKLDPVLSRLKQFSOMNKK 313
Db 252 SDSAKNLIRGMLCSRPSRLTAHLVLRHPWTCENGAVAPDRALDPVLSRLKQFSAMNKK 311
QY 314 KVALRVIAERLSEIEIGLKELFKMIDTNDNGTTITFEELKAGLRKVGSELMESETKSLMD 373
Db 312 QVALRVIAESLSEIEIAGLKEMFKAMDNDNSGATITFELKAGLRKYGTLTKDTEIRDJME 371
QY 374 AADINDSGTIYDGFGLAATLHNKMEREEILVAAPDFDKDGSGYITIDELQSACTEFL 433
Db 372 AADIDKSGTIYDGFGLAATLHNKLEREHLISAFRYFDKDGSGYITIDELQHACAEQGM 431

QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRSRSTMMKNLNFNI 482
Db 432 SDVFLEDVIKEVDQNDGRIDYGEFVAMQKGI-VG--RTMRKSINMSI 477
RESULT 14
T02784
calcium-dependent protein kinase (EC 2.7.1.1-) - maize (strain W64A)
C:Species: Zea mays (maize)
C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 16-Jun-2000
C:Accession: T02784
R:Murillo, I.; Jaeck, E.; Cordero, M.; San Segundo, B.
submitted to the EMBL Data Library, July 1998
A:Description: A calcium-dependent protein kinase possibly involved in pathogen defense
sis-related PRms gene.
A:Reference number: Z14736
A:Accession: T02784
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-639 <MUR>
A:Cross-references: EMBL:AJ007366; PIDN:CAA07481.1
A:Experimental source: strain W64A; seed
C:Function:
A:Description: probably involved in pathogen defense in maize plants
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific;
F:151-411/Domain: protein kinase homology <KIN>
F:159-167/Region: protein kinase ATP-binding motif
F:454-486/Domain: calmodulin repeat homology <EF1>
F:490-522/Domain: calmodulin repeat homology <EF2>
F:526-558/Domain: calmodulin repeat homology <EF3>
F:560-592/Domain: calmodulin repeat homology <EF4>
F:182/Active site: Lys #status predicted

Query Match 64.5%; Score 1672.5; DB 1; Length 639;
Best Local Similarity 66.2%; Pred. No. 2.1e-55;
Matches 318; Conservative 66; Mismatches 83; Indels 13; Gaps 3;
QY 5 PNPR-RPS-----NTVLPYQTPRLRDHYLLGKLGQOGQGTTLCTEKSATSANY 52
Db 120 FSPRPQVQKRVSSAGLLGLSVLRRTKNTLKDYSLGRRLGQGFQGTTLCHVERATGKEL 179
QY 53 ACKSIPKRLKVCREDYEDVVRQIIMHLSHEHPNVVRIKGTYESDVVHVMVECEGGL 112
Db 180 ACKSILKRLKLGSDDDVEDVRRQIIMHLLAGHPSVVGIRGAYED/VAVHLMELCGGEL 239
QY 113 FDRIVSKGHPSEREAVKLITKILGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDF 172
Db 240 FDRIVRRGHYTERKAAELARVIVGVVEACHSMGVNHRDLKPNFLFADHSEEAALKTTIDF 299
QY 173 GLSVFYKPGQYLDVVGSPVYVAPVPLKCKYGPETDVSAGVILYLLSGVPPFWAETES 232
Db 300 GLSIFFRPGQIFTDVVGSPVYVAPVPLKCKYGPEDVWSAGVILYLLSGVPPFWAENRQ 359
QY 233 GIFRQILOGKLDFKSPDMPPTISEAAKDLIYKMLERSPKRISAEALCHPWIVDEQAAPD 292
Db 360 GIFEVLHGLRDFSEPWPSISDGAKOLVRMLVRDPRKRLTAHEVLVRHPWQVGVAPD 419
QY 293 KPLDPAVLSRLKQFSOMNKKIIMHLSHEHPNVVRIKGTYESDVVHVMVECEGGL 352
Db 420 RPLDSAVLSRLKQFSOMNKKIIMHLSHEHPNVVRIKGTYESDVVHVMVECEGGL 479
QY 353 KAGLRKVGSELMESEIEIGLKELFKMIDTNDNGTTITFEELKAGLRKVGSELMESEILVAAPSD 412
Db 480 KVLKGVANLQSEIEIYALMQAADVNNNGTTIDYGEFTAATLHNKVEREDHLFAAFQYFD 539
QY 413 KDGSGYITIDELQSACTEFLGCDTFLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRSR 472
Db 540 KDGSGYITADELQACEFGLGVDQLDGEVDQNDGRIDYNEFVAMQK-PTVGGSR 598
RESULT 15
H84810

probable calcium-dependent protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Mar-2001
C;Accession: H84810
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84810
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-583 <STO>
A;Cross-references: GB:AE002093; NID:g3928078; PIDN:AAC79604.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g38910
A;Map position: 2
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin
C;Keywords: EF hand

Query Match		63.3%	Score 1640.5;	DB 2;	Length 583;
Best Local Similarity		66.9%	Pred. No. 3e-54;		
Matches	307;	Conservative	67;	Mismatches	84;
				Indels	1;
				Gaps	1;
QY	12	NTVLPTQRLRDHYLLGKXGQGFQTTYLCTEKSTANSYACKSIPKRLVCREDEYDV	71		
Db	120	DSVLGRKNTLKDIIYSVGRKLGQGFQTTFLCVDKTKGFEACKTIKRKLTPDEVEDV	179		
QY	72	WREIQIMHLSHPNVIRIKGTVEDSVFVHIMEVCEGGELFDRIVSKGHFSEREAVKLI	131		
Db	180	RREIQIMHLSHPNVIQIVGAYEDAVAVHVMVEICAGGELFDRIIQRGHYTEKAAELA	239		
QY	132	KTILGVVEACHSLGVMHRLKPNFLFDSPKDDAKLKATDFGLSVFYKPGOYLVDVVGSP	191		
Db	240	RIIVGVIEACHSLGVMHRLKPNFLFVSGDEEAAUKTIDFGLSVFPKGETFTDVVGSP	299		
QY	192	YVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQIQKLDKSDPWP	251		
Db	300	YVVAPEVLRKHYSHECDVMSAGVILYLLSGVPPFWDETEQGIQEQLKGLDIFISEPWP	359		
QY	252	TISEAAKDLIYKMLSPKKRISAHEALCHPWIVDQAAAPDKLPDPAVLRLKQFSQMNK	311		
Db	360	SVSESADLVRRMLIIRDPKRMTHIEVLCPHARVDGVGVALDKPLDSAVLSRLQQFSAMNK	419		
QY	312	IKQMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFBELKAGLRKRVGSELMESEIKSL	371		
Db	420	LKKIAIKVIAESLSEEEIAGLKEMFKMIDTNSGHITLBELKGLDRVGDALKDSILGL	479		
QY	372	MDAADIDNSGTTIDYGEFLAATLHMKNKEREELVAAFSDFDKDGSYITIDELQSACTEF	431		
Db	480	MQAADIDNSGTTIDYGEFIAAMVHLNKEIEKEDHLFTAFSYFDQDGSYITRDELQQAQKQF	539		
QY	432	GLCDTFLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGR	470		
Db	540	GLADVHLDDLREVDKNDGRIDYSEFVDM- QDTGFGK	577		

Search completed: November 28, 2003, 10:36:20
Job time : 44 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 28, 2003, 10:31:21 ; Search time 24 Seconds
(without alignments)
969.926 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPSNTVLPYQTP.....KMLNFIADAFGVDEKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1944	75.0	508	1	CDPK SOYBN
2	1724	66.5	610	1	CDP1_ARATH
3	1586	61.2	542	1	CDP3_ORYSA
4	1482	57.2	533	1	CDP2_ORYSA
5	1460.5	56.3	513	1	CDP2_MAIZE
6	1460	56.3	534	1	CDP1_ORYSA
7	1432.5	55.2	532	1	CDPK_DAUCA
8	854	32.9	602	1	CRK_DAUCA
9	591	22.8	499	1	KCCD_HUMAN
10	589.5	22.7	374	1	KCCD_MOUSE
11	589.5	22.7	374	1	KCC1_RAT
12	587.5	22.7	370	1	KCC1_HUMAN
13	578.5	22.3	473	1	KCC4_HUMAN
14	574.5	22.2	533	1	KCCD_RAT
15	574	22.1	469	1	KCC4_MOUSE
16	572	22.1	474	1	KCC4_RAT
17	571.5	22.0	542	1	KCCB_MOUSE
18	569.5	22.0	542	1	KCCB_RAT
19	567.5	21.9	478	1	KCCA_HUMAN
20	566.5	21.8	664	1	KCCB_HUMAN
21	565.5	21.7	478	1	KCCA_RAT
22	549.5	21.2	478	1	KCCA_MOUSE
23	544.5	21.0	529	1	KCCG_MOUSE
24	543.5	21.0	472	1	KCCG_HUMAN
25	539	20.8	527	1	KCCG_RAT
26	534.5	20.6	424	1	KPSH_HUMAN
27	533.5	20.6	386	1	KPSB_HUMAN
28	532.5	20.5	386	1	KPSB_RAT
29	526	20.3	387	1	KPSB_MOUSE
30	524.5	20.2	387	1	KPSB_MOUSE
31	514.5	19.8	295	1	KMLC_DICDI
32	509	19.6	1431	1	DAPK_HUMAN
33	505	19.5	433	1	CDK1_RAT

34	505	19.5	740	1	CDK1_HUMAN
35	505	19.5	756	1	CDK1_MOUSE
36	499	19.2	335	1	KCC1_SCHPO
37	489.5	18.9	752	1	KGAA_CHICK
38	486	18.7	735	1	KGA1_RAT
39	484.5	18.7	512	1	K110_ARATH
40	482.5	18.6	733	1	KGA2_HUMAN
41	481	18.5	724	1	KGA1_MOUSE
42	480	18.5	735	1	KGA1_HUMAN
43	479	18.5	546	1	CHK2_MOUSE
44	477	18.4	733	1	KGAA_XENLA
45	476.5	18.4	733	1	KGA2_MOUSE

ALIGNMENTS

RESULT 1

CDPK_SOYBN

ID CDPK SOYBN STANDARD; PRT; 508 AA.

AC P28583;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calcium-dependent protein kinase SK5 (EC 2.7.1.-) (CDPK).

OS Glycine max (Soybean).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

ON NCBI_TaxID=3847;

RX STRAIN=cv. Williams;

RX MEDLINE=91240279; PubMed=1852075;

RA Harper J.F., Sussman M.R., Schaller G.E., Putnam-Evans C.,

RA Charbonneau H., Harmon A.C.;

RT "A calcium-dependent protein kinase with a regulatory domain similar

RT to calmodulin."

RL Science 252:951-954 (1991)

CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT

CC INVOLVE CALCIUM AS A SECOND MESSENGER.

CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY

CC PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.

CC -!- TISSUE SPECIFICITY: FOUND THROUGHOUT THE PLANT.

CC -!- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN SOYBEAN.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

```
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation.
FT DOMAIN 34 292 PROTEIN KINASE.
FT NP_BIND 40 48 ATP (BY SIMILARITY).
FT BINDING 63 63 ATP (BY SIMILARITY).
FT ACT_SITE 158 158 BY SIMILARITY.
FT CA_BIND 348 359 EF-HAND 1 (POTENTIAL).
FT CA_BIND 384 395 EF-HAND 2 (POTENTIAL).
FT CA_BIND 420 431 EF-HAND 3 (POTENTIAL).
FT CA_BIND 454 465 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 508 AA; 57169 MW; AFCEDC5122419284 CRC64;

Query Match 75.0%; Score 1944; DB 1; Length 508;
Best Local Similarity 77.7%; Pred. No. 5,7e-91;
Matches 370; Conservative 51; Mismatches 51; Indels 4; Gaps 3;

QY 14 VLPVQTPRLRDHYLGGKGGOGFTTLYLCTESTSANYACKSIPKRLKVCREDYEDVWR 73
DB 22 VLPQTNIREVVEVGRKLGOGGFTTCTRASGKGKFAKSIKPKRLKCKEDYEDVWR 81
QY 74 EIQIMHLSHPNVVRIKGTYESVFIHVMVECEGGELEFDRIVSKGHFSEREAVKLKLT 133
DB 82 EIQIMHLSHPNVVRIKGTYESVFIHVMVECEGGELEFDRIVSKGHFSEREAVKLKLT 141
QY 134 ILGVEACHSLGVMHRLDKPENLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193
DB 142 IVEVWEACHSLGVMHRLDKPENLFDSPKDDAKLKATDFGLSVFYKPGESFCFCDVGSPPY 201
QY 194 VAPEVLKCKYCPEDVWSAGVILYLLSGVPPFAETESGIFQILOGKLDKDFSDPWTI 253
DB 202 VAPEVLKCKYCPEDVWSAGVILYLLSGVPPFAETESGIFQILOGKLDKDFSDPWTI 261
QY 254 SEAAKLIYKWLERSPKKRISAHEALCHPWIVDEQAPDKPLDPAPVLSRLKQFSQNMKIK 313
DB 262 SDSAKDLIRKWLQNPTRTLTAHEVLRHPWIVDDNIAPDKPLDPAVLSRLKQFSQNMKIK 321
QY 314 KMAIRVIAERLSSEEGGLKELFMIDTNSGTTITFEELKAGLKRVSSELMSEIKSLMD 373
DB 322 KMAIRVIAERLSSEEGGLKELFMIDTNSGTTITFEELKAGLKRVSSELMSEIKSLMD 381
QY 374 AADIDNSGTTIDYGEFLAATLHMNMKEREILVAAFSDFDKGSGYITIDELQASCTEFG 433
DB 382 AADIDNSGTTIDYGEFLAATLHMNMKEREILVAAFSDFDKGSGYITIDELQASCTEFG 441
QY 434 CDTPLDDMIKEIDLDNDGKIDFSEFTAMRKGD-GVGRSRMTMKNLNFNIADAFV 488
DB 442 DDIHIDMIKEIDLDNDGKIDFSEFTAMRKGD-GVGRSRMTMKNLNFNIADAFV 494

RESULT 2
CDPI_ARATH STANDARD; PRT; 610 AA.
AC Q06850;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase, isoform AK1 (EC 2.7.1.-) (CDPK).
GN AK1 OR AR5G04870 OR MUK11.19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=9313795; PubMed=7916621;
RA Harper J.F., Binder B.M., Sussman M.R.;
RT "Calcium and lipid regulation of an Arabidopsis protein kinase
RL expressed in Escherichia coli.";
RN Biochemistry 32:3282-3290(1993).
RP [2]
RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;
RX MEDLINE=98162728; PubMed=9501997;
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT Sequence features of the regions of 1,191,918 bp covered by seventeen
RL DNA Res. 4:401-414(1997).
CC -1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -1- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY
CC PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -1- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN MOUSE-EAR
CC CRESS.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
CC THIS SWISS-PROT ENTRY IS COPYRIGHT. IT IS PRODUCED THROUGH A COLLABORATION
CC BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION -
CC THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS
CC USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY
CC MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL
CC ENTITIES REQUIRES A LICENSE AGREEMENT (SEE HTTP://WWW.ISB-SIB.CH/ANNOUNCE/
CC OR SEND AN EMAIL TO LICENSE@ISB-SIB.CH).
CC -----
CC EMBL; L14771; AAA32761.1; --
CC EMBL; A8008271; BAB08991.1; --
CC PIR; A49082; A49082.
CC HSSP; P02588; 1PON.
CC InterPro; IPR002048; EF-hand.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR002290; Ser Thr_pkinase.
CC Pfam; PF00036; ehand; 4.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000012; EF-hand; 2.
CC ProDom; PD000001; Prot kinase; 1.
CC SMART; SM00054; Eph; 4.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS00018; EF_HAND; 4.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW Calcium-binding; Phosphorylation; Multigene family.
FT DOMAIN 150 408 PROTEIN KINASE.
FT NP_BIND 156 164 ATP (BY SIMILARITY).
FT BINDING 179 179 ATP (BY SIMILARITY).
FT ACT_SITE 274 274 BY SIMILARITY.
FT CA_BIND 464 475 EF-HAND 1 (POTENTIAL).
FT CA_BIND 500 511 EF-HAND 2 (POTENTIAL).
FT CA_BIND 536 547 EF-HAND 3 (POTENTIAL).
FT CA_BIND 570 581 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 610 AA; 68253 MW; 41868DF12B0DF9FB CRC64;

Query Match 66.5%; Score 1724; DB 1; Length 610;
Best Local Similarity 65.5%; Pred. No. 7,5e-80;
Matches 329; Conservative 62; Mismatches 91; Indels 20; Gaps 2;

QY 2 ETKP-----NPRRP-----SNTVLPYQTPRLRDHYLGGKGGOGFTTY 41
DB 106 ETKPESKDPDPKPKPKMKRVSSAGLRSTESVLQKTKTENFKFYSIGRKLGGQFGTTF 165
QY 42 LCTEKSTSANYACKSIPKRLKVCREDYEDVWEIQLMHLSHPNVVRIKGTYESVFWH 101
DB 166 LCVEKTTGKEFAKSIKRLKLTDEVEDVREIQLMHLAGHPNVISIKGAYEDVVAHV 225
QY 102 IVMVECEGGELEFDRIVSKGHFSEREAVKLKLTILGVWEACHSLGVMHRLDKPENLFDSP 161
DB 226 LWMECCAGGELEFDRIIQGHYTERKAAELTRIVGVWEACHSLGVMHRLDKPENLFDVSK 285
QY 162 KDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLKCKYCPEDVWSAGVILYLLS 221
DB 162 KDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLKCKYCPEDVWSAGVILYLLS 221
```

Db 286 HEDSLKTTIDFGLSMFFKDDVFTDVVGSPPYVAPEVLRRKRYGPEADVMSAGVIVYLLS 345
Qy 222 GVPPFWAETESGIFRLOLQKLDKSDPMTTSEAAKDLIYKMLERSPKKRISAHEALCH 281
Db 346 GVPPFWAETEQGIFEGVLGDDJDFSSDPWPSISAKDLVRKMLVRDPKRLTAHQVLCH 405
Qy 282 PWIVDEQAAPKPLDPAVLRLKQFSQMNKI KKMALRVIAERLSEEEIGGLKELFKVIDT 341
Db 406 PWVQDGVAPDKPLDSAVLSRMKQFSAMNKKFKMALRVIAERLSEEEIAGLKEMFNWIDA 465
Qy 342 DNSGTTTFEELKAGLKRVCSELMESIKSLMDAADIDNSGTTDYGFLAATLHMKNQERE 401
Db 466 DKSQGITFELKAGLKRVCSELMESIKSLMDAADIDNSGTTDYGFLAATLHMKNQERE 525
Qy 402 EILVAAFSDFDKGGSGYITIDELQSACTEFGLCDDTPLDDMIKEIDLDNDGKIDSEFTAM 461
Db 526 DHLFAAFTYFDKGGSGYITIDELQSACTEFGVEDVRIEMLRMDVDQNDGRDYNFVAM 585
Qy 462 MRKGDGVRSTRMKNLNFNIA 483
Db 586 MQKGSITGGPVKMGLEKSFSA 607

RESULT 3

CDP3_ORYSA
ID CDP3_ORYSA STANDARD; PRT; 542 AA.
AC P53684;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Calcium-dependent protein kinase, isoform 11 (EC 2.7.1.-) (CDPK 11).
OS CPK11.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Arborio; TISSUE=Coleoptile;
RX MEDLINE=95284352; PubMed=7766885;
RA Breviario D., Morello L., Giani S.;
RT "Molecular cloning of two novel rice cDNA sequences encoding putative calcium-dependent protein kinases."
RL Plant Mol. Biol. 27:953-967(1995).
CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC -!- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK SUBFAMILY.
CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X81393; CAA57156.1; -.
DR FIR; S56651; S56651.
DR HSP; Q63450; IA06.
DR Gramine; P53684; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; Eph; 3.

SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00018; EF_HAND; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding; Calcium-binding; Phosphorylation; Multigene family.
FT DOMAIN 79 337
FT NP_BIND 81 89 ATP (BY SIMILARITY).
FT BINDING 108 108 ATP (BY SIMILARITY).
FT ACT_SITE 202 202 BY SIMILARITY.
FT DOMAIN 393 404 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 429 440 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT DOMAIN 465 476 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
FT CA_BIND 499 510 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 542 AA; 61166 MW; D4D257275C126DDA CRC64;
Query Match 61.2%; Score 1586; DB 1; Length 542;
Best Local Similarity 63.9%; Pred. No. 5.6e-73;
Matches 304; Conservative 68; Mismatches 102; Indels 2; Gaps 2;
Qy 11 SNTVLPYQTPRLRDHYLLGKLGQGFQGTTLCTEKSSTANVACKSI PKRKLVCREDYED 70
Db 64 SINLGRKTADREHYIIGRKLGGQAFQGTTLCTEINTGCEYACKTIPKRLITKEDVED 123
Qy 71 VVREIQIMHLSHHPNVVRIKGTIEDSVFVHVMVEGEGELFDRIIVSKGHSEAEVKL 130
Db 124 VVREIQIMHLSGHKNVVAIKDYEDGQAVHVMELCAGGELFDRIQEKGHYSERAAEL 183
Qy 131 INTILGVVACHSLGVMHRLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVWGS 190
Db 184 IRIIVSIAMCHSLGVMHRLKPNFLFLDKDDLSIKAKIDFGLSVFYKPGQVFTLVGS 243
Qy 191 PYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRLOLQKLDKSDPW 250
Db 244 PYVAPEVLKRYGPESDVMSAGVILYLLSGVPPFWAETQGGIFDAVLKGHIDFQSDPW 303
Qy 251 PTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPKPLDPAVLRLKQFSQMN 310
Db 304 PKISDSAKDLIRKMLSHCPSERLKAHEVLRHFWICENGVAATQALDPSVISRLKQFSAMN 363
Qy 311 KIKKQALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVCSELMESIEKS 370
Db 364 KLKLLARVIAERLSEEEIAGLRNFKAVDTKNRGVITFGLREGULRRFGAEFKDTEIGD 423
Qy 371 LMDADIDNSGTTDYGFLAATLHMKNQEREELVAAFSDFDKGGSGYITIDELQSACTE 430
Db 424 IMEAAHNNNNVTIHYEEFIAATPLNKIEREHLAAFTYFDKGGSGYITVDKLRACGE 483
Qy 431 FGLCDTPLDDMIKEIDLDNDGKIDSEFTAMMRKRGDVGGRS-RTMMKNLNFNIA 485
Db 484 HNMEDSLJEEIISVDQNDGQIDYAEFVAMM-QQSNVGLGHWQTMESLNLVALRDA 538
RESULT 4
CDP2_ORYSA
ID CDP2_ORYSA STANDARD; PRT; 533 AA.
AC P53683;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Calcium-dependent protein kinase, isoform 2 (EC 2.7.1.-) (CDPK 2).
GN CPK2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Arborio; TISSUE=Coleoptile;
RX MEDLINE=95284352; PubMed=7766885;
RA Breviario D., Morello L., Giani S.;
RT "Molecular cloning of two novel rice cDNA sequences encoding putative


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FT CA_BIND 379 390 EF-HAND 1 (POTENTIAL) .
FT CA_BIND 415 426 EF-HAND 2 (POTENTIAL) .
FT CA_BIND 451 462 EF-HAND 3 (POTENTIAL) .
FT CA_BIND 486 497 EF-HAND 4 (POTENTIAL) .
SQ SEQUENCE 513 AA; 58081 MW; 235A61630C0AC336 CRC64;

Query Match 56.3%; Score 1460.5; DB 1; Length 513;
Best Local Similarity 60.0%; Pred. No. 1e-66;
Matches 276; Conservative 78; Mismatches 105; Indels 1; Gaps 1;

QY 7 PRPNTVLPYQTPRLDRHYLLGKLGQGFQGTTLCTEKTSTANYACKSIPKRLKLVCRE 66
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 46 KPXTADTILGQYEDVRSYSGKELGRGQFGVTLCTEIASGRQYACKSISKRKLVSKA 105
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 67 DYEDVMREIQIMHLSHPNVRIRKGYEDSVFVHIVMEVCEGGEFDRIVSKGHFSERE 126
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 106 DREDIRREIQIMHLSGQPNIVEPRGAYEDKSNVHVMELCAGGELFDRIIAKHGYTERA 165
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 127 AVKLKTLGVVEACHSLGVWHRDLKPNFLDPSKDDAKLKATDFGLSVFKPQOYLVD 186
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 166 AATICRAVNVVNIHFVGVWHRDLKPNFLATMEENAMLKATDFGLSVFIEEGMYRD 225
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 187 VVGSPYVAVPELVKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLPK 246
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 226 IVGSAYVAPVLRYSYKGEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLPK 285
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 247 SDPPTISEAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQF 306
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 286 SQPWPSISSEAKDLVRKMLTRDPKRLTSAQVLOHQLREGEASDKPIDSVAVLRMKQF 345
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 307 SOMNKKIKMARLVIAERLSEIEGKELFKYIDTDSNGTITFEELKAGLRVGSSELMES 366
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 346 RAMNKKIKMARLVIAERLSEIEGKELFKYIDTDSNGTITFEELKAGLRVGSSELMES 405
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 367 EIKSLMDAADLDSNGTIDYGFBLAATLHMNMKEREILVAAFSDPKDGSVITIDELQS 426
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 406 EVKQLMEAADVNGSIDYVEFIATMRHKLDERDEHLFKAFQYFDKNSGFIITRDELES 465
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 427 ACTFGLGCDT-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 466 ALIEHEMGDTSTIREIIEVTDNDGRINYEFCAMMRGG 505
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

RESULT 6

```

CDPI_ORYSA
ID _CDPI_ORYSA STANDARD; PRT; 534 AA.
AC PS3682;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Calcium-dependent protein kinase, isoform 1 (EC 2.7.1.-) (CDPK 1).
GN SPK.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RX MEDLINE=93314961; PubMed=8325505;
RA Kawasaka T., Hayashida N., Baba T., Shinozaki K., Shimada H.;
RT "The gene encoding a calcium-dependent protein kinase located near
RT the sdel gene encoding starch branching enzyme I is specifically
RT expressed in developing rice seeds.";
RL Gene 129:183-189(1993).
CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: SPECIFICALLY EXPRESSED IN SEEDS.
CC -!- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.

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CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL: D13436; BAA02698.1; -.
CC PIR: JCI515; JCI515.
CC HSSP: P02593; ICDM.
CC Gramene: P53682; -.
CC InterPro: IPR002048; EF-hand.
CC InterPro: IPR000719; Prot_Kinase.
CC InterPro: IPR002290; Ser_thr_kinase.
CC Pfam: PF00036; ehand; 4.
CC ProDom: PD000012; EF-hand; 2.
CC ProDom: PD000001; Prot_kinase; 1.
CC SMART: SM00054; EFh_2; 1.
CC SMART: SM00220; S_TKc; 1.
CC PROSITE: PS00018; EF_HAND; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
CC KX Transferase; Serine/threonine-protein kinase; ATP-binding,
CC Calcium-binding; Phosphorylation; Multigene family.
CC KW DOMAIN 73 331 PROTEIN KINASE.
CC FT NP_BIND 79 87 ATP (BY SIMILARITY).
CC FT BINDING 102 102 ATP (BY SIMILARITY).
CC FT ACT_SITE 197 197 BY SIMILARITY.
CC FT DOMAIN 387 398 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
CC FT DOMAIN 422 432 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
CC FT DOMAIN 457 468 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
CC FT CA_BIND 491 502 EF-HAND 4 (POTENTIAL).
CC SQ SEQUENCE 534 AA; 60573 MW; 1932CCD2C4F8C5 CRC64;

```

Query Match 56.3%; Score 1460; DB 1; Length 534;
 Best Local Similarity 59.2%; Pred. No. 1.e-66;
 Matches 280; Conservative 84; Mismatches 105; Indels 4; Gaps 4;

```

QY 14 VLPYQTPRLDRHYLLGKLGQGFQGTTLCTEKTSTANYACKSIPKRLKLVCREYDVMR 73
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 61 VLGYKTPNRELYTLGRELGGQFGKTYLCTEISTGCOYACKTILKSNLRCVSDIEDVRR 120
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 74 EIQMHLHSEHPNVVRIRKGYEDSVFVHIVMEVCEGGEFDRIVSKGHFSEREAVKLK 133
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 121 EIQMHLHSGQKNIVITIKTYEDEQAVHIVMELCAGGELFSKIQKRGHYSERKAAELIKI 180
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 134 ILGVVEACHSLGVWHRDLKPNFLDPSKDDAKLKATDFGLSVFKPQOYLVDVGSPPY 193
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 181 IVGIETCHSGVWHRDLKPNFLDPSKDDAKLKATDFGLSVFKPQOYLVDVGSPPY 240
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 194 VAPEVLKCKYGPEDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLPKDPWPPTI 253
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 241 IAPVLEKRYGPEADITWAGVILYLLSGVPPFWAETESGIFRQILQKLPKDPWPPTI 300
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 254 SEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQMNKIK 313
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 301 SDSAKDLIKMLCPYPLERLKAHEVLKHPWICDNGVATNRALDPSVLPRLKQFSAMNRLK 360
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 314 KMALRVIAERLSEIEGKELFKYIDTDSNGTITFEELKAGLRVGSSELMESIKSLMD 373
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 361 KLSLQIIAERLSEIEGKELFKYIDTDSNGTITFEELKAGLRVGSSELMESIKSLMD 419
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 374 AADINDSGTIDYGFBLAATLHMNMKEREILVAAFSDPKDGSVITIDELQSACTEFLG 433
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 420 AAD-DITSTINWEEFAAAVSLNKIEREKHLMAAFTYFDKDGSGFIITVDLQKACMRNM 478
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKG-DVGRSRMTMKNLNFNIADA 485
   | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

Db 479 EDTFLEEMILEVDQNDQIDYAEFTVMQSNFGLG-WQTVESLNLVALREA 530

RESULT 7

CDPK DAUCA STANDARD; PRT; 532 AA.

AC P28582; ID_CDPK DAUCA STANDARD; PRT; 532 AA.

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calcium-dependent protein kinase (EC 2.7.1.-) (CDPK).

OS Daucus carota (Carrot).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; campanulids; Apiales; Apiaceae; Daucus.

OX NCBI_TaxID=4039;

RN RP SEQUENCE FROM N.A.

RA Choi J.H.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE OF 108-532 FROM N.A.

RX MEDLINE=92003674; PubMed=1912486;

RA Suen K.-L., Choi J.H.;

RT "Isolation and sequence analysis of a cDNA clone for a carrot

RT calcium-dependent protein kinase: homology to

RT calcium/calmodulin-dependent protein kinases and to calmodulin.";

RL Plant Mol. Biol. 17:581-590(1991).

CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT

CC INVOLVE CALCIUM AS A SECOND MESSENGER.

CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY

CC PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CAMK SUBFAMILY.

CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.

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CC -----

DR EMBL; X56599; CAA39936.1; -.

DR FIR; S17759; S17759.

DR FIR; T14335; T14335.

DR HSSP; Q63450; 1A06.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR000719; Prot_kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR Pfam; PF00036; ehand; 4.

DR Pfam; PF00069; pkinase; 1.

DR ProDom; PD000012; EF-hand; 2.

DR ProDom; PD000001; Prot_kinase; 1.

DR SMART; SM00054; EFh; 4.

DR SMART; SM00220; S_TKc; 1.

DR PROSITE; PS00018; EF_HAND; 4.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

DR Transferrase; Serine/threonine-protein kinase; ATP-binding;

KW Calcium-binding; Phosphorylation.

FT DOMAIN 81 339 PROTEIN KINASE.

FT NP_BIND 87 95 ATP (BY SIMILARITY).

FT BINDING 110 110 ATP (BY SIMILARITY).

FT ACT_SITE 205 205 BY SIMILARITY.

FT CA_BIND 395 406 EF-HAND 1 (POTENTIAL).

FT CA_BIND 431 442 EF-HAND 2 (POTENTIAL).

FT CA_BIND 465 476 EF-HAND 3 (POTENTIAL).

FT CA_BIND 500 511 EF-HAND 4 (POTENTIAL).

SQ SEQUENCE 532 AA; 60065 MW; F03E6F036A0AE348 CRC64;

Query Match 55.2%; Score 1432.5; DB 1; Length 532;

Best Local Similarity 59.1%; Pred. No 2.7e-65;

Matches 278; Conservative 76; Mismatches 107; Indels 9; Gaps 5;

QY 2 ETKPN--PR---RP-SNTVLPYQTPRLRDHYLLGKLGQGGQFGTTCCTEKSATSYACK 55

DB 51 QTGPSLKPRQVHRPESNTILGKPFEDIRGKYTLGKELGRQFGCVVQCTENSQQLYACK 110

QY 56 STPKRLKLVREDYEDVWREIQIMHLSSEHPNVVRIKGTYESDVFNHIVMEVCEGGELFDR 115

DB 111 SILKRLKLVSKDKEDIKREIQILOHLSGQPNIVEFGVFEEDRSQVHLVMELCAGGELFDR 170

QY 116 IVSKGHFSREAVKLIKTLGVVEACHSLGVVHRDLKPNFLPDSKDDAKLKATDFGLS 175

DB 171 IIAQGHYSERAAATICRQIVNVVHVCHFGVHRDLKPNFLLSSKDKDAMLKATDFGLS 230

QY 176 VFYKPGQYLYDVGVSPYYVAPEVLKCYCPEDIVWSAGVILYLLSGVPPFWAETESGIF 235

DB 231 VFIEGKVYRNIVGSAYYVAPEVLRYSYGEKDINISAGVILYLLSGVPPFWAENKGF 290

QY 236 ROILOGKLDPKDPWPTISEAAKOLYKMLERSPKKRIISAHEALCHPWIVDEQAADKPL 295

DB 291 DAILEGVIDFSEPEWPSVNSAKDLVRKMLTQDPRRRTTSAQVLDHPWMREGGEASDKPI 350

QY 296 DPAVLSRLKQFSQMNKIKKWLVRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAG 355

DB 351 DSAVLSRMKQFRAMNKLQALKVTAESLSEEEIGGLKSMFANMOTDKSGTITFEELKSG 410

QY 356 LKRVGSELMESEIKSLMDAADINDSGTIDYGFLLATLHMNMKMEREEIILVAAFSDFDKG 415

DB 411 LARLASKLSEVEVQQLMDAADVDGNGTIDYLEFITATMRHKLESYE--HQAFQYFDKDN 468

QY 416 SGVITIDELQSACTEFLCD-TPLDDMIKEIDLNDGKIDFSEFTAMMK 464

DB 469 SGFITVDELSANKEYGMDGDEATIKDIISEVDSNDGRINRYDEFECAMMR 518

RESULT 8

ID CRK DAUCA STANDARD; PRT; 602 AA.

AC P5381;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE CDPK-related protein kinase (EC 2.7.1.-) (PK421).

GN CRK.

OS Daucus carota (Carrot).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; campanulids; Apiales; Apiaceae; Daucus.

OX NCBI_TaxID=4039;

RN [1] SEQUENCE FROM N.A.

RP STRAIN=sv. Juwarot;

RX MEDLINE=95367641; PubMed=7640352;

RA Lindzen E., Choi J.H.;

RT "A carrot cDNA encoding an atypical protein kinase homologous to

RT plant calcium-dependent protein kinases.";

RL Plant Mol. Biol. 28:785-797(1995).

CC -!- DOMAIN: All EF-hand domains seem to be non-functional.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CAMK SUBFAMILY.

CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.

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CC -----

DR EMBL; X83869; CAA58750.1; -.

```

DR PIR: S60052; S60052..
DR HSSP; Q63450; 1A06..
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc_1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
FT Repeat.
FT DOMAIN 20 40 3 X 7 AA TANDEM REPEATS OF S-[LI]-P-X-X-
D-X.
FT REPEAT 20 26 1.
FT REPEAT 27 33 2.
FT REPEAT 34 40 3.
FT DOMAIN 148 410 PROTEIN KINASE.
FT NP_BIND 154 162 ATP (BY SIMILARITY).
FT BINDING 180 180 ATP (BY SIMILARITY).
FT ACT_SITE 276 276 BY SIMILARITY.
FT DOMAIN 465 476 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 502 513 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT DOMAIN 542 553 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
FT DOMAIN 574 585 ANCESTRAL CALCIUM SITE 4 (POTENTIAL).
SQ SEQUENCE 602 AA; 67184 MW; 1D10BF68B37BF447 CRC64;

Query Match 32.9%; Score 854; DB 1; Length 602;
Best Local Similarity 41.2%; Pred. No. 3.2e-36;
Matches 184; Conservative 90; Mismatches 155; Indels 18; Gaps 8;

QY 28 LCKKLGGOGFGTYLCTEKSTSNY-----ACKSIKPKLVCREDYEDVWREIQIMHLS 82
DB 150 VGEVGRGHFG--YTCRAKFKGFKGQDVAVKVIPIKAKMTAIAIEDVRREVKILRALT 207
QY 83 EHPNVVRIRKGTVEDSVFVHVMVCEGCELFDRIVSK-GHFSEREAVKLITLGVVEAC 141
DB 208 GHNNLVQFYDAEDHTNVTVMVWELCEGELLDRILSRGKYTEDDANKVMIOQLNVVAF 267
QY 142 HSLGVNHRDLKPNELFDSPKDKAKLKATDFGLSVFYKPGQYLYDVGVGPPYVVAPEVLKK 201
DB 268 HLQGVVHRLDKPNELFLFKSKEDSQLKATDFGLSDYKVKPDERLNDIVGSAVVAEVLHR 327
QY 202 CYGPEIDWSAGVILYLLSGVPPFAETESGIFROILOGKLDKFDKSDPMTTISEAKDLI 261
DB 328 SYSTADVMSIGVIVSYLLCGSRPFWARTESGIFRAVLKANLSFDPEPPWPSVSEAKDFV 387
QY 262 YKMLERSPKKRISAEALCHPWIVDEQAAPDKPLDPAVLRSRLKQFSQNMKIKKMLRVIA 321
DB 388 KELLNKDPRKRTAAQALCHSWIKNSNDI-KFPLDILVFLMKVYMRSSPLRKAALRALS 446
QY 322 ERLSEEEIGGLKELFMIDTNSGTITPEELKAGLKRVGSELM-ESEIKSLMDAADIENS 380
DB 447 KTLTVDELFLYKEQVLLPEPTKNGTISLENIKQALMRNSTDAMKDSRVLDLVLNALQY 506
QY 381 GTIDYGEFLAATLHNKMER---EELLVAASDFDKGSGVITIDELQSACTEFLGDT 436
DB 507 RMDFEEFCAALSVHQLEALDRWQHARCAVDLFEKQGNRAIMTEELAS---ELGLGFS 563
QY 437 -PLDDMIKEILDNDGKIDFSEFTAMM 462
DB 564 IPVHAVLHDWIRHTDGKLSFLGYVKLL 590

RESULT 9
ID KCED HUMAN STANDARD; PRT; 499 AA.
AC Q13557; O9UGH6; Q9UC09;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II delta chain

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DE (EC 2.7.1.123) (CaM-kinase II delta chain) (CaM kinase II delta
DE subunit) (CaMK-II delta subunit).
DE CAMK2D.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Myocardium;
RX MEDLINE=99205154; PubMed=10189359;
RA Hoch B., Meyer R., Hetzer R., Krause E.-G., Karczewski P.;
RT "Identification and expression of delta-isoforms of the
RT multifunctional Ca2+/calmodulin-dependent protein kinase in failing
RT and nonfailing human myocardium.";
RT Circ. Res. 84:713-721(1999).
RN [2]
RP SEQUENCE OF 1-243 FROM N.A.
RC TISSUE=Insulinoma;
RA Rochlitz H., Voigt A., Lankat-Buttgerit B., Goeke B., Heimberg H.,
RA Nauck M.A., Schiemann U., Schatz H., Pfeiffer A.;
RT "Cloning of the human calcium/calmodulin dependent protein kinase II
RT isoforms in human beta cells.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 302-417 FROM N.A.
RX MEDLINE=97214619; PubMed=9060999;
RA Tombes R.M., Krystal G.W.;
RT "Identification of novel human tumor cell-specific CaMK-II variants.";
RL Biochim. Biophys. Acta 1355:281-292(1997).
CC -!- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN
CC IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -!- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
CC AND DELTA.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Name=Delta 2;
CC IsoId=Q13557-1; Sequence=Displayed;
CC Name=Delta 1;
CC IsoId=Q13557-2; Sequence=Not described;
CC Name=Delta 3;
CC IsoId=Q13557-3; Sequence=Not described;
CC Name=Delta 4;
CC IsoId=Q13557-4; Sequence=Not described;
CC Name=Delta 8;
CC IsoId=Q13557-5; Sequence=Not described;
CC Name=Delta 9;
CC IsoId=Q13557-6; Sequence=Not described;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN CARDIAC MUSCLE AND SKELETAL
CC MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK
CC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF071569; AAD20442.1; --
CC EMBL; AJ252239; CAB65123.1; --
CC EMBL; U50361; AB16866.1; --
CC HSSP; Q63450; 1A06.
CC Genew; HGNC:1462; CAMK2D.
CC GO; GO:0005524; F:ATP binding activity; NAS.
CC GO; GO:0004685; F:calcium/calmodulin-dependent protein kinase. . .; NAS.
CC GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
CC GO; GO:0001558; P:regulation of cell growth; NAS.
CC InterPro; IPR000719; Prot_kinase.

```

DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
 KW Phosphorylation; ATP-binding; Neutrone; Alternative splicing.
 FT DOMAIN 14 272 PROTEIN_KINASE.
 FT NP_BIND 20 28 ATP (BY SIMILARITY).
 FT BINDING 43 43 ATP (BY SIMILARITY).
 FT ACT_SITE 136 136 ATP (BY SIMILARITY).
 FT DOMAIN 291 301 CALMODULIN-BINDING (BY SIMILARITY).
 FT CONFLICT 39 39 G -> E (IN REF. 2).
 SQ SEQUENCE 499 AA; 56297 MW; BBEF0B669A883E65 CRC64;

Query Match 22.8%; Score 591; DB 1; Length 499;
 Best Local Similarity 37.1%; Pred. No. 4.1e-23;
 Matches 142; Conservative 65; Mismatches 144; Indels 32; Gaps 9;

Qy 21 RLDRHYLLGKLGQGGQGGTTLCTEKSTSANVACKSIKPKRLVCRVEDVWREIQIMH 80
 Db 9 RFTDEYQLFEELGKGAFTVRCWKIPGQGYAAKINTKLSAR-DHOKLEREARIC-R 66
 Qy 81 LSEHPNVRIKGTVEDSVFVHIVMEVCEGSELDRIIVSKGHFSEREAVKLITILGVVEA 140
 Db 67 LLKHPNIVRLHDSISEGFHYLVFDLVGTGSELDIVAREYVSEADASHCIQILESVNH 126
 Qy 141 CHSLGVWHRDLKPNFLFDSKDDAKLTKATFGLSVFYKPGQYL-YDVVGSPPYVAPEVL 199
 Db 127 CHLNGIVHRDUPENLLASKSGAAVKLADFGLAIEVQGGQQAQWFGAGTGGYLSPEVL 186
 Qy 200 KK-CYGPEDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLDKLDFKSDPWPTISEAAK 258
 Db 187 RKDPYGPVDMWACGVILYLLGVPPDWDQHLVQIQIKAGAYDPSPPDWIVTPEAK 246
 Qy 259 DLIYKMLERSPKKISAEALCHPWIVDEQAAPDKLPDPAVLRLKQFSQMNKIKKQWALR 318
 Db 247 DLINKMLTINPAKRTASEALKHPWICQSTVASMHRQETVDCLEKFNARRKLKG--A 303
 Qy 319 VIAERLSEEGIGGLKELFKMID-----TDNSG-TITFEELKA---GLKRVGSELMESEIK 369
 Db 304 ILTTLATRFSAKSLKPKDGVKSTESNTTIEDVKARQEIIVKTEQILIEA--- 360
 Qy 370 SLMDAADIDNSGTIDYGEFLAAT 392
 Db 361 -----INNGDFEAYT 370

RESULT 10

KCC1_MOUSE
 ID KCC1_MOUSE STANDARD; PRT; 374 AA.
 AC Q91YS6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)
 DE (CAM kinase I).
 DE CAMK1.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Query Match 22.7%; Score 589.5; DB 1; Length 374;
 Best Local Similarity 41.6%; Pred. No. 3.6e-23;
 Matches 124; Conservative 56; Mismatches 113; Indels 5; Gaps 4;

Qy 18 QTPRLRDHYLLGKLGQGGQGGTTLCTEKSTSANVACKSIKPKRLVCRVEDVWREIQI 77
 Db 12 QAEDIRDIVDFRDLVLTGAFSEVLAEKRTQKLVAKCIAKALEGEG--SWENELAV 69
 Qy 78 MHLSEHPNVRIKGTVEDSVFVHIVMEVCEGSELDRIIVSKGHFSEREAVKLITILGV 137
 Db 70 LHKI-KHPNIVALDDIYESGGHLYLMQLVSGSELDRIIVKGFYTERDASRLIFQVLD 128
 Qy 138 VEACHSLGVWHRDLKPNFLFDSKDDAKLTKATFGLSVFYKPGQYLVDVVGSPYVAPE 197
 Db 129 VKYLDHGLGIVHRDLKPNFLYSLDEDSKIMISDFGLSKMEDGSLVLTACGTPGVVAPE 188
 Qy 198 VL-KCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLDKLDFKSDPWPTISEA 256
 Db 189 VLAQKPYKAVDCWSIGVYAILLCGPPFYDENDAKLFEQILKAEYEDSPWDIDSDS 248
 Qy 257 AKDLIYKMLERSPKKISAEALCHPWIVDEQAAPDKLPDPAVLRLKQFSQMNKIKK 314
 Db 249 AKDFIRHLMEKQPEKRTCEQALQHPWIAGDTAL-DKNIHQSVSEIQIKKFAKSKWKQ 305

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -!- FUNCTION: PHOSPHORYLATES SYNAPSIN I (By similarity).
 CC -!- ENZYME REGULATION: ACTIVATED BY protein = ADP + O-phosphoprotein.
 CC -!- PHOSPHORYLATED TO BE MAXIMALLY ACTIVE.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAMK SUBFAMILY.

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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@sib-sib.ch).

CC EMBL; BC014825; AAH14825.1; -;
 CC MGD; MGI:1098535; Camk1.
 DR InterPro: IPR000719; Prot_kinase.
 DR InterPro: IPR002290; Ser_thr_kinase.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00220; S_TKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
 KW Phosphorylation; ATP-binding.
 FT DOMAIN 20 276 PROTEIN_KINASE.
 FT NP_BIND 26 34 ATP (BY SIMILARITY).
 FT BINDING 49 49 ATP (BY SIMILARITY).
 FT ACT_SITE 141 141 BY SIMILARITY.
 FT MOD_RES 177 177 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 374 AA; 41624 MW; 37889CDA717D3AB2 CRC64;

	Query Match	22.7%; Score 589.5; DB 1;	Length 374;
	Best Local Similarity	41.6%; Pred No. 3.6e-23;	
	Matches 124; Conservative	56; Mismatches 113; Indels	5; Gaps 4
QY	18 QTPRLRHHLLGKKLGGQGFGTTVLTCTEKSTSNAYACKSIPKPKLVCRDYEVDWVREIOI	77	:
Ddb	: : : : : :	:	:
QY	12 QAEDIRDIYDFRVLTGTCAFEVLAEADKRTQKLVAIKTAKALSGKEG--SMENEIAIV	69	:
Ddb	: : : : : :	:	:
QY	78 MHLSSEHPNVVRIGKTGYEDSVFVHI VMEVCCEGGELFDRI VSKGHFSEREAVKLITKILGV	137	:
Ddb	: : : : : :	:	:
QY	70 LHKI-KHPNIVALDDIYESCGHLYLIQLVSGGELFDRIVEKGFTYTERDAERLLIFQVLD	128	:
Ddb	: : : : : :	:	:
QY	138 VEACHSLGVMHRLDKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLVDWGSPYYVAPE	197	:
Ddb	: : : : : :	:	:
QY	129 VKYLHDGI VHRDLKPENLIYYSLEDESKITMISDFGLSKMEDPGSVLSTACTGPGVAPE	188	:
Ddb	: : : : : :	:	:

Qy	198	VL-KKCYGPEDVNSAGVILYILLGSPFPWATETSGIFRQLIQGLDFPKSDPWPPTISEA	255
Dd	189	VLAQPKYSKAVDCDSIGVIAYILLCGYPFYDENDAKUFEQILTKAEYFDPYWDIDIS	248
Qy	257	AKDLTYKNMLERSPKKRIRISAHEALCHPWTVDEQAAPDKPLDPVLSRLKQFSQWNKKK	314
Dd	249	AKDFIRHLMEXDPEKRFCEQALQHPWTAGDTAL-DKNIHQSVSQIKNFAKSKWKQ	305

RESULT 12	
KCC1 HUMAN	
ID KCC1 HUMAN STANDARD; PRT; 370 AA.	
AC Q14012;	
DT 15-JUL-1998 (Rel. 36, Created)	
DT 15-JUL-1998 (Rel. 36, Last sequence update)	
DT 16-OCT-2001 (Rel. 40, Last annotation update)	
DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123)	
DE (CAM kinase I).	
DE DE	
GN CAMK1.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
SEQUENCE FROM N.A.	
RP MEDLINE=95369239; PubMed=7641687;	
RX Haribabu B., Hook S.S., Selbert M.A., Goldstein E.G., Tomhave E.D.,	
RA Edelman A.M., Snyderman R., Means A.R.;	
RT "Human calcium-calmodulin dependent protein kinase I: cDNA cloning,	
RT domain structure and activation by phosphorylation at threonine-177	
RT by calcium-calmodulin dependent protein kinase I kinase.";	
RL EMBO J. 14:3679-3686(1995).	
CC -I- FUNCTION: PHOSPHORYLATES SYNAPSIN I.	
CC -I- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.	
CC -I- ENZYME REGULATION: ACTIVATED BY CA++/CALMODULIN. MUST BE	
CC PHOSPHORYLATED TO BE MAXIMALLY ACTIVE.	
CC -I- SUBUNIT: Monomer.	
CC -I- TISSUE SPECIFICITY: Ubiquitous.	
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.	
CC CAMK SUBFAMILY.	

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DR ENBL; L41816; AAA99458.1; --	
DR PIR; S57347; S57347.	
DR HSSP; Q63450; IA06.	
DR Genev; HGNC:1459; CAMK1.	
DR MIM; 604998; --	
DR GO; GO:0004685; F:calcium/calmodulin-dependent protein kinase. . ; TAS.	
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.	
DR GO; GO:0007165; P:signal transduction; TAS.	
DR InterPro; IPR000719; Prot_kinase.	
DR InterPro; IPR002290; Ser_thr_pkinase.	
DR Pfam; PF00069; pkinase; I.	
DR ProDom; PD000001; Prot_kinase; 1.	
DR SMART; SM00220; S_TKC_1	
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
DR Trnasfaser; Serine/threonine-protein kinase; Calmodulin-binding;	
DR Phosphorylation; ATP-binding; Alternative splicing.	
DR Domain; 20 276 PROTEIN_KINASE	
FT DOMAIN 287 321 CALMODULIN-BINDING (BY SIMILARITY).	
FT NP_BIND 26 34 ATP (BY SIMILARITY).	
FT BINDING 49 49 ATP.	
FT ACT_SITE 141 141 BY SIMILARITY.	
FT MOD_RES 177 177 PHOSPHORYLATION (AUTO-).	
FT FT	

RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedon T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Rutterford S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences".
CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING
CC PROTEIN.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
CC NUCLEI (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q16566-1; Sequence=Displayed;
CC Name=2; Synonyms=Calpermin;
CC IsoId=Q16566-2; Sequence=Not described;
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK
CC SUBFAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; D130742; BAA06403.1; -;
CC DR EMBL; L17000; AAA35639.1; -;
CC DR EMBL; L24959; AAA18251.1; -;
CC DR EMBL; BC016695; AAA18695.1; -;
CC DR PIR; A53036; A53036.
CC DR HSSP; Q63450; 1A06.
CC DR Genew; HGNC:1464; CAMK4.
CC MIM; 114080; -;
CC GO; GO:0004685; F:calcium/calmodulin-dependent protein kinase. . .; TAS.
CC GO; GO:0004688; P:protein amino acid phosphorylation; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR002290; Ser Thr kinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; prot_kinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC PROSITE; PS50011; PROTEIN KINASE DOM; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
CC Calmodulin-binding; Alternative splicing.
CC FT DOMAIN 46 300 PROTEIN KINASE.
CC FT NP_BIND 52 60 ATP (BY SIMILARITY).
CC FT BINDING 75 75 ATP (BY SIMILARITY).
CC FT ACT_SITE 164 164 BY SIMILARITY.
CC FT DOMAIN 322 341 CALMODULIN-BINDING (POTENTIAL).
CC SQ SEQUENCE 473 AA; 51925 MW; EFEE51E5612326DC CRC64;

Query Match 22.3%; Score 578.5; DB 1; Length 473;
Best Local Similarity 37.2%; Pred. No. 1.6e-22;
Matches 140; Conservative 65; Mismatches 144; Indels 27; Gaps 10;

QY 22 LRHYLLGKLGQGFQGTTLCTEKSTSYACKSIPKRLKVCREDYEDVWREIQIMHHL 81
DB 42 LSDFFEVESELGRGATSIYVRCKQKGTQPKYALKVLK-----TVDKKIVRTIGVLLRL 96
QY 82 SEHPNVVRIRKGYVEDSVFVHIVMECEGEGELPDRIIVSKGHFSEAEVKLIKTLGVVEAC 141
DB 97 S-HPNIIKLEKEIETPTETISLVLVLTGGELEFDRIVEKGYISERDAADAVKQILEAVYL 155
QY 142 HSLGVNHRDLKPFENLFDSPKODAKLKATDFGLSVFYKPGQYLYDVVGVPPYVAVELKK 201
DB 156 HENGIVHRDLKENLKYATPADAPLKIADFLGSKIVEHQVLMKTVCGTPGYPGYPELIRG 215
QY 202 C-YGPEIDVMSAGVILYILLGVPFPFAET-ESGIFRQIQGLKDFKSPWPITISEAAKD 259
DB 216 CAYGPEVDMWSGIITILLGFEFPYDERGQDFMFRILNCEYFISPMWDEVSLNADK 275
QY 260 LYKMLERSPKRISAEALCHPWIVDEQAADPKPLDPAVLRLKQFOSOMNKKIKMALRV 319
DB 276 LVKRLIVLDPKRLTTFQALQHPWVTG-KAANFVHMDTA-QKKLOEFNARRKLKAAVKAV 333
QY 320 IA-ERL--SEEEIGGLKELFKM-----IDTNSGTITFEE-----LKAGLKRGVSE 362
DB 334 VASSRLGSSASSHSGSIQESHKASRDPSPIDQGNEDMKAIPEGEKIQDGAQAQAAVKGAAE 393
QY 363 LMSEIKSLMDAADID 378
DB 394 LMKVQALEKVGADIN 409

RESULT 14
KCCD RAT
ID KCCD RAT STANDARD; PRT; 533 AA.
AC P15791;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II delta chain
DE (EC 2.7.1.123) (CaM-kinase II delta chain) (CaM kinase II delta
DE subunit) (CaMK-II delta subunit).
DE CAMK2D.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90036861; PubMed=2553697;
RA Tobimatsu T., Fujisawa H.;
RT "Tissue-specific expression of four types of rat calmodulin-dependent
RL J. Biol. Chem. 264:17907-17912(1989).
RN [2]
RP SEQUENCE OF 314-533 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Aorta, and Skeletal muscle;
RX MEDLINE=93300844; PubMed=8390994;
RA Schworer C.M., Rothblum L.I., Thekkumkara T.J., Singer H.A.;
RT "Identification of novel isoforms of the delta subunit of
RT Ca2+/calmodulin-dependent protein kinase II. Differential expression
RT in rat brain and aorta".
RL J. Biol. Chem. 268:14443-14449(1993).
CC -!- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN
CC IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -!- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
CC AND DELTA.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Delta 1;
CC IsoId=PI5791-1; Sequence=Displayed;
CC Name=Delta 2;
CC IsoId=PI5791-2; Sequence=VSP_004784;
CC Name=Delta 3;

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CC      IsoId=p15791-3; Sequence=VSP_004785, VSP_004786, VSP_004787;
CC      Name=Delta 4;
CC      IsoId=p15791-4; Sequence=VSP_004788;
CC      -!- TISSUE SPECIFICITY: DELTA 1 IS THE PREDOMINANT FORM IN THE BRAIN,
CC      DELTA 2 AND 3 PREDOMINATE IN THE AORTA AND DELTA 4 IN SKELETAL
CC      MUSCLE.
CC      -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK
CC      SUBFAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL; J05072; AAA40866.1; -
CC      EMBL; L13406; AAA41479.1; -
CC      EMBL; L13407; AAA41480.1; -
CC      EMBL; L13408; AAA41481.1; -
CC      PIR; A34366; A34366.
CC      HSP; O63450; 1A06.
CC      InterPro; IPR000719; Prot_kinase.
CC      InterPro; IPR002290; Ser_thr_pkinase.
CC      Pfam; PF00069; pkinase; 1.
CC      ProDom; PD000001; Prot_kinase; 1.
CC      SMART; SM0220; S_TKc; 1.
CC      PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC      PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC      PROSITE; PS00111; PROTEIN KINASE DOM; 1.
CC      Transferrase; Serine/threonine-protein kinase; Calmodulin-binding;
CC      phosphorylation; ATP-binding; Neurone; Alternative splicing.
CC      DOMAIN 14 272 PROTEIN KINASE.
CC      NP_BIND 20 28 ATP (BY SIMILARITY).
CC      BINDING 43 43 ATP (BY SIMILARITY).
CC      ACT_SITE 136 136 BY SIMILARITY.
CC      DOMAIN 291 301 CALMODULIN-BINDING (BY SIMILARITY).
CC      VARSPPLIC 329 362 Missing (in isoform Delta 2).
CC      VARSPPLIC 329 335 INKANV -> KRKSSSV (in isoform Delta 3).
CC      VARSPPLIC 337 359 Missing (in isoform Delta 3).
CC      VARSPPLIC 360 362 GNK -> QMM (in isoform Delta 3).
CC      VARSPPLIC 349 362 Missing (in isoform Delta 4).
CC      SEQUENCE 533 AA; 60080 MW; E41BCB2B5A00E7CA CRC64;
CC      Query Match 22.2%; Score 574.5; DB 1; Length 533;
CC      Best Local Similarity 39.4%; Pred. No. 3e-22;
CC      Matches 127; Conservative 54; Mismatches 134; Indels 7; Gaps 5;
CC
CC      QY 21 RLRDHLLGKLGCGQGTGTYLCTEKSTANYACKSPKRLVCREDYEDVWRQIMMH 80
CC      Db 9 RFTDEYQLFELGKGAFSVVRCMKIPTGQYAAKIINTKLSAR-DHOKLREARIC-R 66
CC
CC      QY 81 LSEHPNVRIKGYEDSVFVHIVNEVCEGELFDRIVSKGHFEREAVKLITLGVVEA 140
CC      Db 67 LLKHPNIVRLHDSISEGFHYLFDLVGTGELFEDIVAREYYSEADASHCIQQLSEVNH 126
CC      QY 141 CHSLGWHRDLKPFENLFDSPKDDAKLKDTPGLSVFYKPGQYL-YDVVGSPYYVAPEVL 199
CC      Db 127 CHLNGIVHRLDKPENLILLASKSGAAVKLADFGLAIEVQDQQAWFAGFTPGYLSPEVL 186
CC      QY 200 KK-CYGEIDVWSAGVLYLTLSSGPPFAETESGIFRQILQKLPKSPDPTISEAK 258
CC      Db 187 RKDPYKPKDVMWACGVLYLILVGYPPFDEQHRLYQQIKAGAYDFPSPEDTDTVTPK 246
CC      QY 259 DLYIKMLERSPKKRIISAHEALCHPWIIVDEQAQPKLDPKLVRLKQFSQMNKIKKWLAR 318
CC      Db 247 DLINKMLTINPAKRITASEALKHPWICQRTVASMHRQETVDCCLKFNARRKLKG---A 303
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QY 319 VIAERLSEEEIGGLKELFKMID 340
Db 304 ILTMTLATRNFSAAKSLKKPD 325
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RESULT 15

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KCC4_MOUSE
ID_KCC4_MOUSE STANDARD; PRT; 469 AA.
AC P08414; Q61381;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type IV catalytic chain
DE (EC 2.7.1.123) (CAM kinase-GR) (CaMK IV).
DE CAMK4.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=91372388; PubMed=1893997;
RA Jones D.A., Giod J., Wilson-Shaw D., Hahn W.E., Sikela J.M.;
RT "cDNA sequence and differential expression of the mouse
RL Ca2+/calmodulin-dependent protein kinase IV gene.";
RN [2]
RX MEDLINE=240-469 FROM N.A.
RX MEDLINE=89122027; PubMed=2536634;
RA Sikela J.M., Law M.L., Kao P.-T., Hartz J.A., Wei Q., Hahn W.E.;
RT "Chromosomal localization of the human gene for brain
RL Ca2+/calmodulin-dependent protein kinase type IV.";
RN [3]
RX SEQUENCE OF 315-469 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87204263; PubMed=3033675;
RA Sikela J.M., Hahn W.E.;
RT "Screening an expression library with a ligand probe: isolation and
RL sequence of a cDNA corresponding to a brain calmodulin-binding
protein.";
RN [4]
RX Proc. Natl. Acad. Sci. U.S.A. 84:3038-3042 (1987).
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
CC NUCLEI.
CC -!- TISSUE SPECIFICITY: BRAIN AND TESTIS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -----
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CC -----
CC EMBL; M16206; AAA39933.1; -
CC EMBL; M64266; AAA37364.1; -
CC EMBL; J03057; AAA37366.1; -
CC EMBL; X58995; CAA41741.1; -
CC PIR; S17656; S17656.
CC HSP; Q63450; 1A06.
CC MGD; MGI:88258; Camk4.
CC GO; GO:0016563; F:transcriptional activator activity; IMP.
CC GO; GO:0007270; P:nervous system synaptic transmission; IMP.
CC GO; GO:0006468; P:protein amino acid phosphorylation; IMP.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
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Search completed: November 28, 2003, 10:32:03
Job time : 26 secs

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OM protein - protein search, using sw model

Run on: November 28, 2003, 10:31:21 ; Search time 26 Seconds
(without alignments)
805.534 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPSNTVLPYQTP.....KNLNFNIADAFGVGKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Parents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1927	74.3	463	1 US-07-951-715A-25	Sequence 25, Appl
2	1927	74.3	463	2 US-08-459-448A-25	Sequence 25, Appl
3	1927	74.3	463	3 US-08-459-595A-25	Sequence 25, Appl
4	1927	74.3	463	3 US-08-459-504B-25	Sequence 25, Appl
5	1927	74.3	463	3 US-08-459-444-25	Sequence 0, Appli
6	1927	74.3	463	4 US-09-547-422-25	Sequence 0, Appli
7	1672.5	64.5	639	3 US-09-347-801-17	Sequence 17, Appl
8	1437.5	55.4	464	1 US-07-951-715A-22	Sequence 22, Appl
9	1437.5	55.4	464	2 US-08-459-448A-22	Sequence 22, Appl
10	1437.5	55.4	464	3 US-08-459-595A-22	Sequence 22, Appl
11	1437.5	55.4	464	3 US-08-459-504B-22	Sequence 22, Appl
12	1437.5	55.4	464	3 US-08-459-444-22	Sequence 0, Appli
13	1437.5	55.4	464	4 US-09-547-422-22	Sequence 0, Appli
14	1277.5	49.3	408	1 US-07-951-715A-21	Sequence 21, Appl
15	1277.5	49.3	408	2 US-08-459-448A-21	Sequence 21, Appl
16	1277.5	49.3	408	3 US-08-459-595A-21	Sequence 21, Appl
17	1277.5	49.3	408	3 US-08-459-504B-21	Sequence 21, Appl
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19	1277.5	49.3	408	4 US-09-547-422-21	Sequence 21, Appl
20	829	32.0	623	3 US-09-347-801-4	Sequence 4, Appli
21	826	31.9	525	3 US-09-347-801-18	Sequence 4, Appli
22	800	30.9	576	3 US-09-347-801-19	Sequence 18, Appl
23	771.5	29.8	456	1 US-08-464-164-2	Sequence 19, Appl
24	771.5	29.8	456	1 US-08-338-057-2	Sequence 2, Appli
25	771.5	29.8	456	2 US-08-668-416-2	Sequence 2, Appli
26	622	24.0	520	4 US-09-257-825B-20	Sequence 20, Appl
27	587.5	22.7	370	2 US-08-878-989-19	Sequence 19, Appl

Sequence 19, Appl
Sequence 31, Appl
Sequence 21, Appl
Sequence 10, Appl
Sequence 19, Appl
Sequence 4, Appli
Sequence 2, Appli
Sequence 18, Appl
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Sequence 3, Appli
Sequence 3, Appli
Sequence 30, Appl
Sequence 5, Appli
Sequence 5, Appli
Sequence 23, Appl
Sequence 23, Appl

28 587.5 22.7 370 3 US-09-272-796-19
29 587.5 22.7 370 4 US-09-457-040B-31
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31 554 21.4 355 4 US-09-579-664B-10
32 548 21.1 284 2 US-07-857-224B-19
33 543.5 21.0 556 4 US-09-800-960-4
34 539 20.8 565 4 US-09-800-960-2
35 538 20.7 264 2 US-07-857-224B-18
36 535.5 20.7 424 2 US-08-715-568A-1
37 533.5 20.6 387 1 US-08-713-828-3
38 533.5 20.6 387 2 US-08-919-627-3
39 533.5 20.6 387 2 US-09-096-245-3
40 533.5 20.6 387 4 US-09-457-040B-30
41 532.5 20.5 343 2 US-08-878-989-5
42 532.5 20.5 343 3 US-09-272-796-5
43 530 20.4 295 1 US-07-951-715A-23
44 530 20.4 295 2 US-08-459-448A-23
45 530 20.4 295 3 US-08-459-595A-23

ALIGNMENTS

RESULT 1
US-07-951-715A-25
; Sequence 25, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlino, Ellis J.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
OTHER INFORMATION: soybean CDPK as shown in Figure 34."
US-07-951-715A-25

Query Match 74.3%; Score 1927; DB 1; Length 463;
Best Local Similarity 78.7%; Pred. No. 1.3e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

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QY 14 VLPYQTPRLRDHYLLGKLGQGGQFGTTYLCTEKSTSAANYACKSIPKRLKLVCREYEDVWR 73
Db 1 VLPQRTQNIREVVEVGRKLGQGGQFGTTCTRRASGGKFAKSIIPKRLKLVCKEDYEDVWR 60
QY 74 EIQIMHHLSEHPNVRIKGTYESDVFVHIVMEVCEGELFDRIVSKGHFSERAVKLIKT 133
Db 61 EIQIMHHLSEHANVRIEGTYEDSTAVHLVMECEGELFDRIVKGHYSERQAARLIKT 120
QY 134 ILGVVEACHSLGVMHRLDKPENFLFDSPKDDAKLKATDFGLSVFYKPGQVLYDVVGSPYY 193
Db 121 IVEVVEACHSLGVMHRLDKPENFLFDTIDEDAKLKATDFGLSVFYKPGSFCDVVGSPYY 180
QY 194 VAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWPPTI 253
Db 181 VAPEVLKLYGPESDVMSAGVILYLLSGVPPFWAETESGIFRQILGLKDFHSEWPSSI 240
QY 254 SEAAKDLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMKIK 313
Db 241 SDSAKDLIRKMLDQNPKTRLTAEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAMNKLK 300
QY 314 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFBELKAGLKRVGSELMSEIKSLMD 373
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QY 374 AADIDNSGTDYGEFLAATLHMKVREELVAFSDFDKGSGYITIDELQSACTEFLG 433
Db 361 AADIDKSGTDYGEFIAATVHLNKLREENLVSAFSDYDKGSGYITLDEIQQACKDFGL 420
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMK 476
Db 421 DDIIHDDMIKEIDQDNDGQIDYGEFAAMRKNGGIGR-RTMRK 463
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RESULT 2

US-08-459-448A-25
Sequence 25, Application US/08459448A
Patent No. 5859336

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Croesland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
OTHER INFORMATION: soybean CDPK as shown in Figure 34."
US-08-459-448A-25

Query Match 74.3%; Score 1927; DB 2; Length 463;
Best Local Similarity 78.7%; Pred. No. 1.3e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

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QY 14 VLPYQTPRLRDHYLLGKLGQGGQFGTTYLCTEKSTSAANYACKSIPKRLKLVCREYEDVWR 73
Db 1 VLPQRTQNIREVVEVGRKLGQGGQFGTTCTRRASGGKFAKSIIPKRLKLVCKEDYEDVWR 60
QY 74 EIQIMHHLSEHPNVRIKGTYESDVFVHIVMEVCEGELFDRIVSKGHFSERAVKLIKT 133
Db 61 EIQIMHHLSEHANVRIEGTYEDSTAVHLVMECEGELFDRIVKGHYSERQAARLIKT 120
QY 134 ILGVVEACHSLGVMHRLDKPENFLFDSPKDDAKLKATDFGLSVFYKPGQVLYDVVGSPYY 193
Db 121 IVEVVEACHSLGVMHRLDKPENFLFDTIDEDAKLKATDFGLSVFYKPGSFCDVVGSPYY 180
QY 194 VAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWPPTI 253
Db 181 VAPEVLKLYGPESDVMSAGVILYLLSGVPPFWAETESGIFRQILGLKDFHSEWPSSI 240
QY 254 SEAAKDLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQMKIK 313
Db 241 SDSAKDLIRKMLDQNPKTRLTAEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAMNKLK 300
QY 314 KMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFBELKAGLKRVGSELMSEIKSLMD 373
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Db 301 KVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTDELKDLKRGVSELMSESEIKDLMD 360
QY 374 AADINSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKGSGYITIDELQSACTEFG 433
Db 361 AADIDKSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKGSGYITIDELQSACTEFG 420
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
Db 421 DDHIDDDMIKEIDQNDGQIDYGEFAAMMRKGNNGGIGR-RTMRK 463

RESULT 3

US-08-459-595A-25
; Sequence 25, Application US/08459595A
; Patent No. 6018104

GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, John L.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 6018104artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005

COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/459.595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.

; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..463

; OTHER INFORMATION: /note= "protein sequence for

; OTHER INFORMATION: soybean CDPK as shown in Figure 34."

US-08-459-595A-25

Query Match

Best Local Similarity 74.3%; Score 1927; DB 3; Length 463;

Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPYQTPRLRDHYLLGKKGQGFQTTTCTKTSANVACKSIPKRLKVCREDYEDVNR 73

Db 1 VLPQRTQNIREVYEVGRKLGQGFQTTCTRAGGRFACKSIPKRLKVCREDYEDVNR 60

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Db 61 EIQIMHILSEHANVVRIEGTYEDSTAVHLVMECEGELFDRIVKSGHFSEAEVKLIK 120

QY 134 ILGVVEACHSLGVMEHDLKPNFLFDSKDDAKLKTDFGLSVFYPKQGYLYDVVGSPPY 193

Db 121 IVEVVEACHSLGVMEHDLKPNFLFDTTDEDAKLKATDFGLSVFYPKQGYLYDVVGSPPY 180

QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFMAETESGIFRQILQGLDFKSDPWP 253

Db 181 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFMAETESGIFRQILQGLDFKSDPWP 240

QY 254 SEAAKDLTYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSOMNK 313

Db 241 SDSAKDLIRKMLDQNPKRLTAHEVLRHPWIVDDNIAPDKPLDPAVLSRLKQFSOMNK 300

QY 314 KVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTDELKDLKRGVSELMSESEIKDLMD 373

Db 301 KVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTDELKDLKRGVSELMSESEIKDLMD 360

QY 374 AADINSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKGSGYITIDELQSACTEFG 433

Db 361 AADIDKSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKGSGYITIDELQSACTEFG 420

QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476

Db 421 DDHIDDDMIKEIDQNDGQIDYGEFAAMMRKGNNGGIGR-RTMRK 463

RESULT 4

US-08-459-504B-25

; Sequence 25, Application US/08459504B

; Patent No. 6075185

GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, John L.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: No. 6075185artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park

STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
soybean CDPK as shown in Figure 34."
US-08-459-504B-25

Query Match 74.3%; Score 1927; DB 3; Length 463;

Best Local Similarity 78.7%; Pred. No. 1.3e-152;

Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPTQPLRLDRHYLLGKLGQGGFTTYLCTEKSTSANVACKSIIPKRLVCREDYEDVWR 73
Db 1 VLPTQPLRLDRHYLLGKLGQGGFTTYLCTEKSTSANVACKSIIPKRLVCREDYEDVWR 60
QY 74 EIQIMHLLSEHPNVRIKGTYESVVFHIVMEVCEGGLFDRIVSKGHFSREAVKLKLT 133
Db 61 EIQIMHLLSEHPNVRIKGTYESVVFHIVMEVCEGGLFDRIVSKGHFSREAVKLKLT 120
QY 134 ILGVVACHSLGVMHRLDLPENFLDPSPKDDAKLKATDGLSVFYKPGQYLDVVGSPYY 193
Db 121 ILGVVACHSLGVMHRLDLPENFLDPSPKDDAKLKATDGLSVFYKPGQYLDVVGSPYY 180
QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWTI 253
Db 181 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWTI 240
QY 254 SAAAKDLIYKMLERSPKKISAEALCHPWIVDEQAAPDKLPDPAVLRLKQFSQMNKTK 313
Db 241 SAAAKDLIYKMLERSPKKISAEALCHPWIVDEQAAPDKLPDPAVLRLKQFSQMNKTK 300
QY 314 KVALRVIAERLSEEEIGGLKELFKMTDNTSGTITFEELKAGLKRVSSELSLMD 373
Db 301 KVALRVIAERLSEEEIGGLKELFKMTDNTSGTITFEELKAGLKRVSSELSLMD 360
QY 374 AADINSGTIDYGEFLAATLHMNMEREELVAAFSDFDKGSGYITIDELQSACTEFL 433
Db 361 AADINSGTIDYGEFLAATLHMNMEREELVAAFSDFDKGSGYITIDELQSACTEFL 420

QY 434 CDTPLDDMIKEIDLNDGKIDSEFTAMMRKGD-GVGRSRSTMMK 476
Db 421 DDIIHDDMIKEIDLNDGQIDYGEFAAMMRKGGIGR-RTMRK 463

RESULT 5

US-08-459-444-25
Sequence 0, Application US/08459444A
Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,444A

FILING DATE: 02-Jun-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: /note= "protein sequence for
soybean CDPK as shown in Figure 34."

SEQUENCE CHARACTERISTICS:

LENGTH: 463 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-459-444-25

Query Match 74.3%; Score 1927; DB 3; Length 463;

Best Local Similarity 78.7%; Pred. No. 1.3e-152;

Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPTQPLRLDRHYLLGKLGQGGFTTYLCTEKSTSANVACKSIIPKRLVCREDYEDVWR 73
Db 1 VLPTQPLRLDRHYLLGKLGQGGFTTYLCTEKSTSANVACKSIIPKRLVCREDYEDVWR 60

Db 1 VLPQTQNIREVYEVGRKLGQGGQGTTFECTRRASGGKFACKSIPKRLCKEDYEDVWR 60
QY 74 EIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGELEFDRIYVSKGHFSREAVKLIKT 133
Db 61 EIQIMHLSHANVVRLEGTYEDSTAVHLMELCEGGELEFDRIYVSKGHFSREAVKLIKT 120
QY 134 ILGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193
Db 121 IVEVVEACHSLGVNHRDLKPNFLFDIDEDAKLKATDFGLSVFYKPGSECDVVGSPPY 180
QY 194 VAPVLKCKYGPEDVMSAGVILYLLSGVPPFWAETESGIFROILOGKLDKFDSDPWTI 253
Db 181 VAPVLKCKYGPEDVMSAGVILYLLSGVPPFWAETESGIFROILOGKLDKFDSDPWTI 240
QY 254 SEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAKPLDPAVLRLKQFSOMNKK 313
Db 241 SDSAKDLIRKMLDQNPTRTLTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAMNKK 300
QY 314 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSELMSEIKSLMD 373
Db 301 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSELMSEIKSLMD 360
QY 374 AADIDNSGTTIDYGEFLAATLHMNMKEREELVAAFSDFKDGGSGYITIDELOSACTEGL 433
Db 361 AADIDNSGTTIDYGEFLAATLHMNMKEREELVAAFSDFKDGGSGYITIDELOSACTEGL 420
QY 434 CDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
Db 421 DDHIDDDMIKEIDQDNDGQIDYGEFAAMMRKGGIGR-RTMRK 463

RESULT 6

US-09-547-422-25
; Sequence 0, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lydie D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: /note= "protein sequence for
; soybean CDPK as shown in Figure 34."
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..463
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-547-422-25

Query Match 74.3%; Score 1927; DB 4; Length 463;
Best Local Similarity 78.7%; Pred. No. 1.3e-152;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;
QY 14 VLPQTQNIREVYEVGRKLGQGGQGTTFECTRRASGGKFACKSIPKRLCKEDYEDVWR 73
Db 1 VLPQTQNIREVYEVGRKLGQGGQGTTFECTRRASGGKFACKSIPKRLCKEDYEDVWR 60
QY 74 EIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGELEFDRIYVSKGHFSREAVKLIKT 133
Db 61 EIQIMHLSHANVVRLEGTYEDSTAVHLMELCEGGELEFDRIYVSKGHFSREAVKLIKT 120
QY 134 ILGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193
Db 121 IVEVVEACHSLGVNHRDLKPNFLFDIDEDAKLKATDFGLSVFYKPGSECDVVGSPPY 180
QY 194 VAPVLKCKYGPEDVMSAGVILYLLSGVPPFWAETESGIFROILOGKLDKFDSDPWTI 253
Db 181 VAPVLKCKYGPEDVMSAGVILYLLSGVPPFWAETESGIFROILOGKLDKFDSDPWTI 240
QY 254 SEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAKPLDPAVLRLKQFSOMNKK 313
Db 241 SDSAKDLIRKMLDQNPTRTLTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAMNKK 300
QY 314 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSELMSEIKSLMD 373
Db 301 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSELMSEIKSLMD 360
QY 374 AADIDNSGTTIDYGEFLAATLHMNMKEREELVAAFSDFKDGGSGYITIDELOSACTEGL 433
Db 361 AADIDNSGTTIDYGEFLAATLHMNMKEREELVAAFSDFKDGGSGYITIDELOSACTEGL 420
QY 434 CDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
Db 421 DDHIDDDMIKEIDQDNDGQIDYGEFAAMMRKGGIGR-RTMRK 463

RESULT 7

US-09-347-801-17
; Sequence 17, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97

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; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Zea mays
US-09-347-801-17

Query Match      64.5%; Score 1672.5; DB 3; Length 639;
Best Local Similarity 66.2%; Pred. No. 3.3e-131;
Matches 310; Conservative 66; Mismatches 83; Indels 13; Gaps 3;

QY 5  PNPR-RPS-----NTVLPYQTPRLRDHYLLGKLGQGGTGYLCTEKSATSANY 52
Db 120 PSRPRPOVKRVSSAGLLGSLVLRKNTENLKDYSGLRRLGQGGTGYLCTEKSATSANY 179
QY 53 ACKSPKPKLVCREYEDVWREIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGEL 112
Db 180 ACKSLKRLKSGDDVDVREIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGEL 239
QY 113 FDRIVSKGHFSEREAVKLIKITLGVVEACHSGVNMHRLKPNFLFDSPKDDAKLKATDF 172
Db 240 FDRIVRRGHYTERKAAELARVIVGVVEACHSGVNMHRLKPNFLFADHSEEAALKTTDF 299
QY 173 GLSVFYKPGQVLYDVVVGSPYVAVPEVLKCKYCPEDVMSAGVILYILLSGVPPFWAETES 232
Db 300 GLSIFFRGQIFTDVVGSPYVAVPEVLKCKYCPEDVMSAGVILYILLSGVPPFWAETES 359
QY 233 GIFRQILQGLKDFSDPMTPTISEAAKOLIVKMLERSPKKRISAHEALCHPMIVDEQAAPD 292
Db 360 GIFEEVLHGRLDSESEWPSISDGAOLVRLMLYRDPKRLTAHEVLRHPVQGVVAPD 419
QY 293 KPLDPVLSRLKQFSQNMKI KKMALRVIAERLSBEEIGGLKELFKMIDTNSGTTTPEEL 352
Db 420 RPLDSAVLSRLKQFSQNMKI KKMALRVIAERLSBEEIGGLKELFKMIDTNSGTTTPEEL 479
QY 353 KAGLKRVGSELMSESEIKSLMDAADDNSGTTIDYGEFLAATLHMNMKREETLVAAFSDPD 412
Db 480 KVGLEKVGANLQSEIYALMQAADVNNGTIDYGEFLAATLHMNMKREETLVAAFSDPD 539
QY 413 KDGSGYITIDELQACTEFGCLDTPDDMIKEIDLNDGKIDFSEFTAMMRKGQGVGRSR 472
Db 540 KDGSGYITADELQACEBFGCLDQLEDLIGEDVDQDNDGRIDYNEFVAMMQK-PTVGSR 598

RESULT 8
US-07-951-715A-22
; Sequence 22, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; NUMBER OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA

; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; NAME/KEY: Protein
; LOCATION: 1..464
; OTHER INFORMATION: /note= "derived protein sequence of
; OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-07-951-715A-22

Query Match      55.4%; Score 1437.5; DB 1; Length 464;
Best Local Similarity 60.9%; Pred. No. 8.4e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRHYLLGKLGQGGTGYLCTEKSATSANYACKSLKRVLCREYEDVWREIQIMHHL 81
Db 9 VRATYSMGKELGRGQGVTHLCTHRTSGEKLACKTIARKLAAREDDVDRREVIQIMHHL 68
QY 82 SEHPNVVRIKGTVEDSVFVHIVMEVCEGELFDRIVSKGHFSEREAVKLIKITLGVVEAC 141
Db 69 SGQPNVVLGRGAYEDKOSVHLVMELCAGGELFDRITARGQYTERGAELLRATVQIVHTC 128
QY 142 HSLGVNMHRLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQVLYDVVVGSPYVAVPEVLK 201
Db 129 HSMGVNMHRLKPNFLFDSKDEADAPLKATDFGLSVFFKEGELLARDIVGSAYYIAPEVLK 188
QY 202 CYGPEIDVMSAGVILYILLSGVPPFWAETESGIFRQILQGLKDFPKSDPMTPTISEAAK 261
Db 189 KYGPEADIVMSAGVILYILLSGVPPFWAETESGIFRQILQGLKDFPKSDPMTPTISEAAK 248
QY 262 YKMLERSPKKRISAHEALCHPMIVDEQAAPDKPLDPAVLRLKQFSQNMKI KKMALRVIA 321
Db 249 KQMLNINPKRLTAQVLRHPVWKEDGADPTDNDVLRDLKQFRANNOFKKALRLRIA 308
QY 322 ERLSEBEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVGSELMSESEIKSLMDAADDNSG 381
Db 309 GCLSEBEEITGLKEMFNKIDKNSGTTITLDELKHLAKHGPKLSDSEMEKLEAADAAGNG 368
QY 382 TIDYGEFLAATLHMNMKREETLVAAFSDPKDQSGYITIDELQACTEFGCLDTP-PLDD 440
Db 369 LIDYDEFVATVHMNMKLDREELHYTAFQYDFDKDNGSYITKEELEHALKEQGLYDADKID 428
QY 441 MIKEIDLNDGKIDFSEFTAMMRKG 465
Db 429 IISDADSDNDGRIDYSEFVAMMRKG 453

RESULT 9
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US-08-459-448A-22
; Sequence 22, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..464
; OTHER INFORMATION: /note= "derived protein sequence of
; OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-08-459-448A-22
Query Match 55.4%; Score 1437.5; DB 2; Length 464;
Best Local Similarity 60.9%; Pred. No. 8.4e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;
22 LRDHVLLGKLGQGGTTLCTERSTSNACKSIPKRLVCREDYEDVWREIQIMHHL 81

Db 9 VRATYSMGKELGRGQFGVTHLCTHRTSGEKLACKTKIAKRLAAREDDVDVRRVQIMHHL 68
QY 82 SEHPNVRRIKGYEDSVFVHIWNEVCEGEGELPDRIIVSKGHFSREAVKLIKTLGVVEAC 141
Db 69 SGQPNVVLGRGAYEDKQSVHLMELCAGGELPDRIIARGQYTERGAELRAIVQIVHTC 128
QY 142 HSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFVKPGQYLYDVVGVSPYYVAPEVLKK 201
Db 129 HSMGVNHRDIKPNFLLSKDEDAPLKATDFGLSVFVKEGELLRDVGSAIYIAPVLR 188
QY 202 CYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQIQLOGLKDFKSDPMTTISEAAKDLI 261
Db 189 KYGPEADIMSVGMVLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPMWPHISPGAKDLV 248
QY 262 YWMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFQOMKIKKMAALRVIA 321
Db 249 KXMLNINPKERLTAFQVLNHPWIKEDGDAPDPTPLDNVWLDRLKQFRAMNQFKAALRIIA 308
QY 322 ERLSEEEIGLKLKELFKMIDTNSGTITFEELKAGLRVGSSELMESEIKSIMDAADIDNSG 381
Db 309 GCLSEEEITGLKEMFNKIDKNSGTITLDELKHLAKHGPJKLSDSEWEKLEMAADADNG 368
QY 382 TIDYGEFLAATLHMNMKEREELVAAFSDFDKDGGYITIDELQSACTEFGLCDT-PLDD 440
Db 369 LIDYDEFVTATVMNKLDRHEHLYTAFQYFDKNSGYITKEELEHALKEQGLYDADKID 428
QY 441 MIKEDLDNDGKIDFSEFTAMMRKG 465
Db 429 IISDADSDNDGRIDYSEFVAMMRKG 453

RESULT 10
US-08-459-595A-22
; Sequence 22, Application US/08459595A
; Patent No. 6018104
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6018104artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..464
; OTHER INFORMATION: /note= "derived protein sequence of
; OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-08-459-448A-22

PRIOR APPLICATION DATA:
APPLICANT: Kramer, Vance C.
FILING DATE: 25-SEP-1992
PRIORITY DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /note= "derived protein sequence of
US-08-459-595A-22

Query Match 55.4%; Score 1437.5; DB 3; Length 464;
Best Local Similarity 60.9%; Pred. No. 8.4e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRHYLLGKLGKGGQFGTTLCTEKSISANYACKSIPKRLVCREYEDVWREIQIMHHL 81
DB 9 VRATYSMGKELGRGQGVTHLCTHRTSGEKLACKTIKRLAAREDDVDRREVQIMHHL 68
QY 82 SEHPNVVRIKGTYESVFIHVEVCEGGELEFDRIVSKGHFSERAVKLIKTLGVVEAC 141
DB 69 SGQPNVGLRGAYEDKQSVHLMELCAGGELFDRIIARGQYTERGAELLRAIVQIVHTC 128
QY 142 HSLGVMRDLKPNFLPDSKDDAKLKTATDFGLSVFPGQYLVVGVSPYVAPVLLK 201
DB 129 HSMGVMRDLKPNFLLSKDDAPLKTATDFGLSVFKEGELLRDIVGSAYYIAPVLLK 188
QY 202 CYPEIDVAGVILYLLSGVPPFWAETSGIFRQILQKGLDFKSPWPTISEAAKDLI 261
DB 189 KYGPEADIVSGVMLYIFLAGVPPFWAENENGIFTALRGQLDLSSEPPWPHISPGAKDLV 248
QY 262 YKMLERSPKRISAEALCHPWIVDEQAAPDKPLDPVLSRLKQFSQMNKIKKVALRVIA 321
DB 249 KKMNLNPKRLTAFQVNLHPWIKEDGDAPDTPLDNVVLDRLKQFRANNOFKKAALRIIA 308
QY 322 ERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKRVSSELMSEIKSLMDAADINDSG 381
DB 309 GCLSEEBITGLKEMFKNDKNSGTITLDELKHLAKHGPKLSDSEMEKLEAARDADGNG 368
QY 382 TIDYGEPLAATLHNKMERELIIVAPSDPDKGSGVITIDELQSACTEFLGCDT-PLDD 440
DB 369 LIDYDEFVATVHMKLDREHLYTAFQYFDKNSGYITKEELEHALKEQGLYDADKID 428
QY 441 MIKEIDLNDGKIDFSEFTAMMRKG 465
DB 429 IISDADSDNDGRIDYSEFVAMMRKG 453

RESULT 11
US-08-459-504B-22
Sequence 22, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.

APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launis, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patencin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 464 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..464
OTHER INFORMATION: /note= "derived protein sequence of
US-08-459-504B-22

Query Match 55.4%; Score 1437.5; DB 3; Length 464;
Best Local Similarity 60.9%; Pred. No. 8.4e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRHYLLGKLGKGGQFGTTLCTEKSISANYACKSIPKRLVCREYEDVWREIQIMHHL 81
DB 9 VRATYSMGKELGRGQGVTHLCTHRTSGEKLACKTIKRLAAREDDVDRREVQIMHHL 68
QY 82 SEHPNVVRIKGTYESVFIHVEVCEGGELEFDRIVSKGHFSERAVKLIKTLGVVEAC 141
DB 69 SGQPNVGLRGAYEDKQSVHLMELCAGGELFDRIIARGQYTERGAELLRAIVQIVHTC 128


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; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: /note= "derived protein sequence of
; pollen specific CDPK as disclosed in Figure 34."
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; NAME/KEY: Protein
; LOCATION: 1..464
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-547-422-22

Query Match      55.4%;   Score 1437.5;   DB 4;   Length 464;
Best Local Similarity 60.9%;   Pred. No. 8.4e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY    22 LRDHVLGKLGCGQGFTYLCTSEKTSANYACKSIPKLVCREYEDVWREIQIMHHL 81
Db     :|::||::||::||::||::||::||::||::||::||::||::||::||::||
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QY    82 SEHPNVVRIKGTYESDVSVHIVMEVSCGGELFDRI VSKGHFSEREAVKLTKTLGVVEAC 141
Db     ||::||::||::||::||::||::||::||::||::||::||::||::||
          69 SGQENVVGLRGAYEDKGSVHLVMELCAGGELFDRIARGQYTERGAELRLAIVQIWHTC 128
QY    142 HSLGVMRDLPENFLPDSKODAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKK 201
Db     ||::||::||::||::||::||::||::||::||::||::||::||::||
          129 HSMGWHRDIKPENFLLLSKDEDAPLKATDFGLSVFFKEGELLRDIVGSAYIIAPEVLKR 188
QY    202 CYGPIDWSAGVILTYILLSGVPFPFAETESGI FRQLLOGKLDPKSDPWPTISEAAKDLI 261
Db     ||::||::||::||::||::||::||::||::||::||::||::||::||
          189 KYGPEADINSGVMWLYIFLAGVPFPFAENENGIFTAILRGQLDLSSFWPHISFGAKDLV 248
QY    262 YKMERSPKRIRISAHEALCPHWIVDEQAAPDKPLDPAVLSRLKQFSOMNKIKMALRVIA 321
Db     ||::||::||::||::||::||::||::||::||::||::||::||::||
          249 KKMNLINPKERLTAFQVLNHPWKEDGDAPDTPLDNVVDRLKQFRAMNQFKAAURLIA 308
QY    322 ERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLRKVGSSELMESEIKSLMDAADINDSG 381
Db     ||::||::||::||::||::||::||::||::||::||::||::||::||
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QY    382 TIDYGFBFLAATLHNKMEREEILVAAFSDFKDGSGVITTIDELQSACTEFGLCDT-PLDD 440
Db     ||::||::||::||::||::||::||::||::||::||::||::||::||
          369 LIDYDEFVATVHNKLDREHLYTAFOYFDKONSGITKEELEHALKGQGLYDADKIKD 428

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Qy      441 MIKEIDLNDGKIDFSEFTAMMRKG 465
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Db      429 IISDADSNDGRIDYSEFVAMMRKG 453

RESULT 14
US-07-951-715A-21
; Sequence 21, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Malini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Marlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCES FOR THE TREATMENT OF INSECTICIDAL ACTIVITY
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Ver 1.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-Sep-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/C/O
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 408 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-951-715A-21

Query Match          49.3%; Score 1277
Best Local Similarity 61.9%; Pred. No.
Matches 242; Conservative 59; Mismatch 10

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Db      1 QIMHLLSGQPNVVLGRGAYEDKQSVDLVMEVC 100

Qy      136 GVUYEACHSLGVWHDLKPENELFDSPKDDAA 160

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QY 256 AAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFQSNKTKKM 315
Db 181 GAKDLVKQMLNINPKERLTAFQVLNHPWIKEDGDAPDTPLDNVVLDRKQFRANMQFKA 240
QY 316 ALRVIAERLSEEEIGGKELFKMIDTNSGTITFEELKAGLKRVGSELMSEIKSLMDAA 375
Db 241 ALRIIAGCLSEEEITGLKEMFNKIDKNSGTITLDELKGLAKHGPKLSDSEMEKLEMAA 300
QY 376 DIDNSGTIDYGEFLAATLHMNMKMEREBILVAAFSDFDKDGSYITIDELQSACTEFLGLCD 435
Db 301 DADGNGLIDYDEFVTATVHMNKLDRHEHLYTAFQYFDKNSGYITKEELEHALKEQGLYD 360
QY 436 T-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465
Db 361 ADKIKDIISDADSDNDGRIDYSEFVAMMRKG 391

RESULT 15

US-08-459-448A-21
; Sequence 21, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403

; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 408 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-459-448A-21

Query Match 49.3%; Score 1277.5; DB 2; Length 408;
Best Local Similarity 61.9%; Pred. No. 1.5e-98;
Matches 242; Conservative 59; Mismatches 89; Indels 1; Gaps 1;

QY 76 QIMHHLSEHPNVRIKGTVEDSVFVHVMVEVCGGELFDRIVSKGHFSEAEVAKLIKIL 135
Db 1 QIMHHLGGQPNVVGLRGAYEDKQSVHLVMELCAGGELFDRIIARGQYTERGAALLRAIV 60
QY 136 GVVEACHSLGVHRDLKPNFLFDSPKDDAKLAKATDFGLSVFVKPGQYLYDVVGSPPVVA 195
Db 61 QIVHTCHSMGMVHRDIKPNFLLSKDEDAPLKATDFGLSVFFKEGELLRDIVGSAYIIA 120
QY 196 PEVLKCKYCGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGLDFKSDPWPTISE 255
Db 121 PEVLKRYGPEADIVSWGVMLYIFLAGVPPFWAENENGIFTALRGQLDLSSEFPWPHISP 180
QY 256 AAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFQSNKTKKM 315
Db 181 GAKDLVKQMLNINPKERLTAFQVLNHPWIKEDGDAPDTPLDNVVLDRKQFRANMQFKA 240
QY 316 ALRVIAERLSEEEIGGKELFKMIDTNSGTITFEELKAGLKRVGSELMSEIKSLMDAA 375
Db 241 ALRIIAGCLSEEEITGLKEMFNKIDKNSGTITLDELKGLAKHGPKLSDSEMEKLEMAA 300
QY 376 DIDNSGTIDYGEFLAATLHMNMKMEREBILVAAFSDFDKDGSYITIDELQSACTEFLGLCD 435
Db 301 DADGNGLIDYDEFVTATVHMNKLDRHEHLYTAFQYFDKNSGYITKEELEHALKEQGLYD 360
QY 436 T-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465
Db 361 ADKIKDIISDADSDNDGRIDYSEFVAMMRKG 391

Search completed: November 28, 2003, 10:36:55

Job time : 27 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model
Run on: November 28, 2003, 10:35:37 ; Search time 259 Seconds
(without alignments)
352.507 Million cell updates/sec

Title: US-09-848-806-1
Perfect score: 2593
Sequence: 1 METKNPRRPSNTVLPYQTP.....KNLFNFIADAFGVDGKSD 495

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues
Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/FCI_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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 - 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/2/pubpaa/FCIUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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 - 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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 - 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2593	100.0	495	12	US-10-289-172-1
2	2593	100.0	495	12	US-09-848-806-1
3	2458	94.8	501	12	US-10-289-172-3
4	2458	94.8	501	12	US-09-848-806-3
5	1927	74.3	463	11	US-09-988-462-25
6	1672.5	64.5	639	10	US-09-854-731-17
7	1509.5	58.2	549	9	US-09-828-313-39
8	1437.5	55.4	464	11	US-09-988-462-22
9	1277.5	49.3	408	11	US-09-988-462-21
10	849	32.7	597	9	US-09-828-313-38
11	829	32.0	623	10	US-09-854-731-4
12	826	31.9	625	10	US-09-854-731-18
13	800	30.9	576	10	US-09-854-731-19
14	591	22.8	499	12	US-10-354-358-88
15	587.5	22.7	317	11	US-09-935-464-36

16	587.5	22.7	317	15	US-10-125-835-36	Sequence 36, Appli
17	587.5	22.7	370	10	US-09-817-181-4	Sequence 4, Appli
18	587.5	22.7	370	12	US-09-769-970-19	Sequence 19, Appli
19	587.5	22.7	370	12	US-10-090-002-4	Sequence 4, Appli
20	587.5	22.7	370	12	US-10-204-041-10	Sequence 10, Appli
21	587.5	22.7	370	15	US-10-142-356-7	Sequence 7, Appli
22	587.5	22.7	370	15	US-10-300-828-4	Sequence 4, Appli
23	578.5	22.3	473	12	US-10-320-351-15	Sequence 15, Appli
24	578.5	22.3	473	12	US-10-116-275-153	Sequence 153, Appli
25	566.5	21.8	516	12	US-09-820-790-2	Sequence 2, Appli
26	566.5	21.8	542	12	US-09-820-790-4	Sequence 4, Appli
27	554	21.4	355	12	US-10-355-975-10	Sequence 10, Appli
28	554	21.4	357	15	US-10-024-036B-2	Sequence 2, Appli
29	543.5	21.0	556	14	US-10-096-960-4	Sequence 4, Appli
30	543	20.9	460	11	US-09-935-464-3	Sequence 3, Appli
31	543	20.9	460	15	US-10-125-835-3	Sequence 3, Appli
32	543	20.9	476	11	US-09-935-464-5	Sequence 5, Appli
33	543	20.9	476	15	US-10-125-835-5	Sequence 5, Appli
34	539	20.8	565	14	US-10-096-960-2	Sequence 2, Appli
35	538.5	20.8	326	10	US-09-817-181-2	Sequence 2, Appli
36	538.5	20.8	326	12	US-10-090-002-2	Sequence 2, Appli
37	538.5	20.8	326	15	US-10-300-828-2	Sequence 2, Appli
38	537	20.7	254	11	US-09-898-837A-38	Sequence 38, Appli
39	533.5	20.6	387	10	US-09-771-161A-188	Sequence 188, Appli
40	532.5	20.5	343	12	US-09-769-970-5	Sequence 5, Appli
41	530	20.4	295	11	US-09-988-462-23	Sequence 23, Appli
42	510.5	19.7	648	15	US-10-024-036B-5	Sequence 5, Appli
43	510.5	19.7	817	10	US-09-992-481-4	Sequence 4, Appli
44	510.5	19.7	817	12	US-10-434-034-4	Sequence 4, Appli
45	509	19.6	1431	12	US-10-352-684A-38	Sequence 38, Appli

ALIGNMENTS

RESULT 1
US-10-289-172-1
; Sequence 1, Application US/10289172
; Publication No. US20030154504A1
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: Calcium Dependent Protein Kinase
; FILE OF INVENTION: Polyptides as Regulators of Plant Disease Resistance
; FILE REFERENCE: 00786/389002
; CURRENT APPLICATION NUMBER: US/10/289,172
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/201,925
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-289-172-1

Query Match	100.0%	Score 2593	DB 12	Length 495
Best Local Similarity	100.0%	Pred. No. 2.9e-187	Mismatches 0	Indels 0
Matches 495	Conservative 0			Gaps 0
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Db	1	METKNPRRPSNTVLPYQTPRLRDHYLLGKLGQGFQGTYYLCTEKSTANTACKSIPKR	60	
QY	61	KLVCREDYEDVWREIQIMHHLSEHPNVRIKGTYESVVFHVIMEVCEGELFDRIVSKG	120	
Db	61	KLVCREDYEDVWREIQIMHHLSEHPNVRIKGTYESVVFHVIMEVCEGELFDRIVSKG	120	
QY	121	HFSREAEVKLTKTLGVVEACHSLGWMRDLPENFLDPSPKDDAKLKATDGLSVFYKYP	180	
Db	121	HFSREAEVKLTKTLGVVEACHSLGWMRDLPENFLDPSPKDDAKLKATDGLSVFYKYP	180	
QY	181	GQYLDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFFMAETESGIFQILQ	240	

Db 181 GOYLYDVVGSPPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 240
Qy 241 GKLDKSDPWPPTTISEAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL 300
Db 241 GKLDKSDPWPPTTISEAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL 300
Qy 301 SRLKQFSQMNKIKKQALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVG 360
Db 301 SRLKQFSQMNKIKKQALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVG 360
Qy 361 SELMESEIKSLMDAADIDNSGTTIDYGEFLAATLHMNMKWEREELVAAFPDCKDGSYIT 420
Db 361 SELMESEIKSLMDAADIDNSGTTIDYGEFLAATLHMNMKWEREELVAAFPDCKDGSYIT 420
Qy 421 IDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRGSRRTWMKNLNF 480
Db 421 IDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRGSRRTWMKNLNF 480
Qy 481 NIADAFGVGDKSD 495
Db 481 NIADAFGVGDKSD 495

RESULT 2
US-09-848-806-1
; Sequence 1, Application US/09848806
; Publication No. US20030167516A1
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: Calcium Dependent Protein Kinase
; TITLE OF INVENTION: Polypeptides as Regulators of Plant Disease Resistance
; FILE REFERENCE: 00786/389002
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/201,925
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-848-806-1

Query Match 100.0%; Score 2593; DB 12; Length 495;
Best Local Similarity 100.0%; Pred. No. 2.9e-187;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 METKPNRRSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTLCTEKSTSYACKSIPKR 60
Db 1 METKPNRRSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTLCTEKSTSYACKSIPKR 60
Qy 61 KLVCREYEDVWREIQIMHHLSEHPNVVRIKGTYESVVFVHIVMEVCEGELFDRIVSKG 120
Db 61 KLVCREYEDVWREIQIMHHLSEHPNVVRIKGTYESVVFVHIVMEVCEGELFDRIVSKG 120
Qy 121 HFSEBAVLKILITGLVVEACHSLGVNHRDLKPENFLDPSKDDAKLKATDFGLSVFYKP 180
Db 121 HFSEBAVLKILITGLVVEACHSLGVNHRDLKPENFLDPSKDDAKLKATDFGLSVFYKP 180
Qy 181 GOYLYDVVGSPPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 240
Db 181 GOYLYDVVGSPPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 240
Qy 241 GKLDKSDPWPPTTISEAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL 300
Db 241 GKLDKSDPWPPTTISEAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL 300
Qy 301 SRLKQFSQMNKIKKQALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVG 360
Db 301 SRLKQFSQMNKIKKQALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVG 360

Qy 361 SELMESEIKSLMDAADIDNSGTTIDYGEFLAATLHMNMKWEREELVAAFPDCKDGSYIT 420
Db 361 SELMESEIKSLMDAADIDNSGTTIDYGEFLAATLHMNMKWEREELVAAFPDCKDGSYIT 420
Qy 421 IDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRGSRRTWMKNLNF 480
Db 421 IDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRGSRRTWMKNLNF 480
Qy 481 NIADAFGVGDKSD 495
Db 481 NIADAFGVGDKSD 495

RESULT 3
US-10-289-172-3
; Sequence 3, Application US/10289172
; Publication No. US20030154504A1
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: Calcium Dependent Protein Kinase
; TITLE OF INVENTION: Polypeptides as Regulators of Plant Disease Resistance
; FILE REFERENCE: 00786/389002
; CURRENT APPLICATION NUMBER: US/10/289,172
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/201,925
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 501
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-289-172-3

Query Match 94.8%; Score 2458; DB 12; Length 501;
Best Local Similarity 94.8%; Pred. No. 4.4e-177;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

Qy 4 KPNRRPSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTLCTEKSTSYACKSIPKRKL 63
Db 3 KPNRRPSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTLCTEKSTSYACKSIPKRKL 62
Qy 64 CREDYEDVWREIQIMHHLSEHPNVVRIKGTYESVVFVHIVMEVCEGELFDRIVSKGHFS 123
Db 63 CREDYEDVWREIQIMHHLSEHPNVVRIKGTYESVVFVHIVMEVCEGELFDRIVSKGCF 122
Qy 124 EREAVLKILITGLVVEACHSLGVNHRDLKPENFLDPSKDDAKLKATDFGLSVFYKPGQY 183
Db 123 EREAAKLKILITGLVVEACHSLGVNHRDLKPENFLDPSKDDAKLKATDFGLSVFYKPGQY 182
Qy 184 LYDVVGSPPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 243
Db 183 LYDVVGSPPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 242
Qy 244 DFKSDPWPPTTISEAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL 303
Db 243 DFKSDPWPPTTISEAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL 302
Qy 304 KQFSQMNKIKKQALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVGSEL 363
Db 303 KQFSQMNKIKKQALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVGSEL 362
Qy 364 MESEIKSLMDAADIDNSGTTIDYGEFLAATLHMNMKWEREELVAAFPDCKDGSYITIDE 423
Db 363 MESEIKSLMDAADIDNSGTTIDYGEFLAATLHMNMKWEREELVAAFPDCKDGSYITIDE 422
Qy 424 LQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRGSRRTWMKNLNF 483
Db 423 LQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRGSRRTWMKNLNF 482
Qy 484 DAFGVGDKSD 495
Db 483 EAFGVGDKSD 498

RESULT 4
US-09-848-806-3
; Sequence 3, Application US/09848806
; Publication No. US20030167516A1
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: Calcium Dependent Protein Kinase
; FILE REFERENCE: Polypeptides as Regulators of Plant Disease Resistance
; CURRENT APPLICATION NUMBER: US/09/848,806
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/201,925
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; TYPE: PRT
; LENGTH: 501
; ORGANISM: Arabidopsis thaliana
US-09-848-806-3

Query Match 94.8%; Score 2458; DB 12; Length 501;
Best Local Similarity 94.8%; Pred. No. 4.4e-177;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

QY 4 KNPSPSTVLPYQTPRLRDHYLLGKLGQGFQGTYYLCTEKSTSAHYACKSIPKRLV 63
DB 3 KNPSPSTVLPYQTPRLRDHYLLGKLGQGFQGTYYLCTEKSTSAHYACKSIPKRLV 62

QY 64 CREDYEDVWREIQIMHLSHPNVRIKGYEDSVFVHVMVEVCEGELFDRIVSKGHS 123
DB 63 CREDYEDVWREIQIMHLSHPNVRIKGYEDSVFVHVMVEVCEGELFDRIVSKGHS 122

QY 124 EREAVKLITLGVVEACHSLGVMHRLDKPENFLDPSKDDAKLKATDFGLSVFVKPGQY 183
DB 123 EREAVKLITLGVVEACHSLGVMHRLDKPENFLDPSKDDAKLKATDFGLSVFVKPGQY 182

QY 184 LYDVVGSPPYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIPRQILQGL 243
DB 183 LYDVVGSPPYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIPRQILQGL 242

QY 244 DFKSDPWTITSEAKDLIKMLERSPKRISAHEALCHPWIVDEQAAPKPLDPAVLSRL 303
DB 243 DFKSDPWTITSEAKDLIKMLERSPKRISAHEALCHPWIVDEQAAPKPLDPAVLSRL 302

QY 304 KQFSQMKIKKVALRVIAERLSEEEIGGLKELFKMIDTDSNGTITFEELKAGLKRVSSEL 363
DB 303 KQFSQMKIKKVALRVIAERLSEEEIGGLKELFKMIDTDSNGTITFEELKAGLKRVSSEL 362

QY 364 MESEIKSLMDAADTNSGTIDYGEFLAATLHNMKMERBEILVAFSDFDKSGVITIDE 423
DB 363 MESEIKSLMDAADTNSGTIDYGEFLAATLHNMKMERBEILVAFSDFDKSGVITIDE 422

QY 424 LQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEPTAMRKGDGVRGSRRTMMKNLFNIA 483
DB 423 LQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEPTAMRKGDGVRGSRRTMMKNLFNIA 482

QY 484 DAFGVGDS----EKSDD 495
DB 483 EAFGVEDTSSTAKSD 498

RESULT 5
US-09-988-462-25
; Sequence 25, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.

Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauais, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-No. US20030046726A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 463 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Protein
LOCATION: 1..463
OTHER INFORMATION: /note= "protein sequence for
soybean CDPK as shown in Figure 34."
SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-988-462-25

Query Match 74.3%; Score 1927; DB 11; Length 463;
Best Local Similarity 78.7%; Pred. No. 4.1e-137;
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPYQTPRLRDHYLLGKLGQGFQGTYYLCTEKSTSAHYACKSIPKRLVCREYEDVWR 73
DB 1 VLPQRTQNIREVYEVGRKLGQGFQGTYYLCTEKSTSAHYACKSIPKRLVCKEDYEDVWR 60

QY 74 EIQIMHLSHPNVRIKGYEDSVFVHVMVEVCEGELFDRIVSKGHSREAVKLKT 133
DB 61 EIQIMHLSHPNVRIKGYEDSVFVHVMVEVCEGELFDRIVSKGHSREAVKLKT 120

QY 134 ILGVVEACHSLGVMHRLDKPENFLDPSKDDAKLKATDFGLSVFVKPGQYLYDVVGSPPY 193
DB 121 IVEVVEACHSLGVMHRLDKPENFLDPSKDDAKLKATDFGLSVFVKPGQYLYDVVGSPPY 180

Qy 194 VAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLDKFSKDPWPTI 253
Db 181 VAPEVLKLYGPESDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLDKFSKDPWPSI 240
Qy 254 SEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAAPDPLDPAVLRLKQFSQMKIK 313
Db 241 SDSAKDLIRKWLDOONPKTRTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAMNKLK 300
Qy 314 KMALRVIAERLSSEIEIGLKFQKIDTNSGTTTFEELKAGLKRVSSELSSEIKSLMD 373
Db 301 KMALRVIAERLSSEIEIGLKFQKIDTNSGTTTFEELKAGLKRVSSELSSEIKSLMD 360
Qy 374 AADIDNSGTTDYGEFLAATLHMNMKEREIEILVAAFSDFDKGSGYITIDELQSACTEFL 433
Db 361 AADIDKSGTTIDYGEFLAATLHMNMKEREIEILVAAFSDFDKGSGYITIDELQSACTEFL 420
Qy 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMK 476
Db 421 DDHIDDDMIKEIDQNDGQIDYGEFAAMMRKNGGIGR-RTMRK 463

RESULT 6
US-09-854-731-17
; Sequence 17, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Zea mays
US-09-854-731-17

Query Match 64.5%; Score 1672.5; DB 10; Length 639;
Best Local Similarity 66.2%; Pred. No. 9.3e-118;
Matches 318; Conservative 66; Mismatches 83; Indels 13; Gaps 3;

Qy 5 PNPRPQVKRVSSAGLLGSLVLRKTENLKQKYLGRLLGQGFQGTTHLCVERATGKEL 179
Db 120 PSRPRPQVKRVSSAGLLGSLVLRKTENLKQKYLGRLLGQGFQGTTHLCVERATGKEL 179
Qy 53 ACKSIPKRLVCRDEDVWREIQIMHLSSEHPNVVRIRKGYEDSVFVHIVMEVCBGGEL 112
Db 180 ACKSILKRLGSDDDVEDVRREIQIMHLAGHPSVVGIRGAYEDAVAVHLVMELCGGEL 239
Qy 113 FRIIVSKGHFSREAAVKLITLGVVEACHSLGVMHRLDKPENFLFDSPKDDAKLKATDF 172
Db 240 FRIIVRGHYTERKAAELARVIVGVVEACHSGVMHRLDKPENFLFDSHSEAAALKTIDF 299
Qy 173 GLSVFYKPGQYLYDVVSGPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETES 232
Db 300 GLSIFRPQGIPTDVVSGPYVAPEVLKCYGPEADVMSAGVILYLLSGVPPFWAENBQ 359
Qy 233 GFRQILQKLDKFSKDPWPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAAPD 292
Db 360 GIFEVLHGRDLFSEEPWPSISDGAIDLVRRLVDRPDKRLTAHEVLRHPWVQGVAPD 419
Qy 293 KPLDPAVLRLKQFSQMKIKMALRVIAERLSSEIEIGLKFQKIDTNSGTTTFEEL 352
Db 420 RPLDSAVLSRLKQFSAMNKLKMALRVIAERLSSEIEIGLKFQKIDTNSGTTTFEEL 479
Qy 353 KAGLKRVSSELSSEIKSLMDAADIDNSGTTIDYGEFLAATLHMNMKEREIEILVAAFSDFD 412
Db 480 KVGLKVGANLQESBIYALMQAADVDNNGTTIDYGEFLAATLHNLKVEREDHLFAAFQYFD 539

Qy 413 KDGSGYITIDELQSACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVCGRSR 472
Db 540 KDGSGYITADELQVACEEFGLDGVEDQNDGRIDYNEFVAMMQK-PTVGGSR 598

RESULT 7
US-09-828-313-39
; Sequence 39, Application US/09828313
; Patent No. US20020059662A1
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: THIELEN, NOCHA VAN
; APPLICANT: CHEN ROUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-313-39

Query Match 58.2%; Score 1509.5; DB 9; Length 549;
Best Local Similarity 60.8%; Pred. No. 1.5e-105;
Matches 290; Conservative 70; Mismatches 112; Indels 5; Gaps 3;

Qy 5 PNPRPSNT---VLPYQTPRLRDHYLLGKLGQGFQGTTYLCTEKSATSANYACKSIPKRR 61
Db 69 PRPKPASRSVSGVLGKPLSDIRQSYILGRELGRQFGVYILCTDKMTNEAYACKSIKRR 128
Qy 62 LYCREDEYDWRREIQIMHLSSEHPNVVRIRKGYEDSVFVHIVMEVCBGGELFRIIVSKGH 121
Db 129 LTKSEDIEDVREKREVQIMHLSGTPNIWLVKDFEDKHSVHLMELCAGGELFRIIVAKGH 188
Qy 122 FSREARVLIKTIILGVVEACHSLGVMHRLDKPENFLFDSPKDDAKLKATDFGLSVFKPG 181
Db 189 YSERAADMCVRIVNVVHRLCHSLGVFHRDLKPFENFLAASKAEDAPDKATDFGLSTFFKPG 248
Qy 182 QYLYDVVSGPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 241
Db 249 DVFQDIVGSAYYVAPEVLKRSYGPADVMSAGVIVVILLCGVPPFWAETEQGIFDAVLKG 308
Qy 242 KLDFKSDPWPPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAAPDPLDPAVL 301
Db 309 HIDFENDPMPKISNGAKDLVRKMLPNVKIRLTAQOVLNHPNMKEDGADPDVPLDNAVL 368
Qy 302 RLKQFSQMKIKMALRVIAERLSSEIEIGLKFQKIDTNSGTTTFEELKAGLKRVS 361
Db 369 RLKNSAANKMKLAKVIAESLSSEIEIGLKFQKIDTNSGTTTFEELKAGLKRVS 428
Qy 362 ELMESEIKSLMDAADIDNSGTTIDYGEFLAATLHMNMKEREIEILVAAFSDFDKGSGYIT 421
Db 429 KLNESDIRKLEAADVNGKIDFNEFISATMHNMKTEKEDHLMAAFHFDFTDNGSYIT 488
Qy 422 DELQSACTEFLGCD-TPPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476
Db 489 DELOAMEKNGMDPETTIEIISVDTDNGRIDYDEFVAMMRKNGPGAENGCTVKN 545

RESULT 8
US-09-988-462-22
; Sequence 22, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:

QY	142	HSLGVMHRDLKPNFLFDSKPKDAKLRATDGLSVFYKPGQYLYDVVVGSPYYVAPEVLKK	201
Db	129	HSMSGVMHRDIKPNFLLLSKDEADAPLAKATDGLSVFPKKEGELLARDIVGSAYYIAPEVLKR	188
QY	202	CYGPEDVWSAGVILYILLSGVPPFWAETESGIFRQILQOKLDFKSDPWPWTISEAAKDLI	261
Db	189	KYGPEDADWSVGVMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPWPPIHISPGAKDLV	248
QY	262	YKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVL SRLKQFOSOMNKIKKALRVIA	321
Db	249	KKMLNINPKERLTAFQVNLHPWIKEDGADPTPLDNLVLDRLQKFRAMNOFKKAALRIIA	308
QY	322	ERLSEEEIGGLKELFKMIDTNSCTITFEELKAGLRKXVSGELMESEIKSLMDAADIDNSG	381
Db	309	GCLSEEBITGLKEMFKNIDKDNSCTITLDELKHLGAKHGPKLSDSEWKLMEAADADGNG	368
QY	382	TIDYGEFLAATLHNKMERBEILVAAPSDFKDQSGYITIDELQSACTEFLGCDT-PLDD	440
Db	369	LIDYDEFVTATVHNKLDREEHLYTAFQYFDKDNSGYITKEELEHALKEOGLYDADKID	428
QY	441	MIKEIDLNDGKIDFSEFTAMMRKG	465
Db	429	IISDADSDNDGRIDYSEFVAMMRKG	453
RESULT 9			
US-09-988-462-21			
; Sequence 21, Application US/09988462			
; Publication No. US20030046726A1			
; GENERAL INFORMATION:			
; APPLICANT: Koziel, Michael G.			
; Desai, Nalini M.			
; Lewis, Kelly S.			
; Kramer, Vance C.			
; Warren, Gregory W.			
; Evola, Stephen V.			
; Crossland, Lyle D.			
; Wright, Martha S.			
; Merlin, Ellis J.			
; Launis, Karen L.			
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED			
INSECTICIDAL ACTIVITY IN MAIZE			
NUMBER OF SEQUENCES: 94			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Syngenta Biotechnology, Inc.			
STREET: 3054 Cornwallis Road			
CITY: Research Triangle Park			
STATE: NC			
COUNTRY: USA			
ZIP: 27709			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent in Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/988,462			
FILING DATE: 20-NOV-2001			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 09/547,422			
FILING DATE: 11-APR-2000			
APPLICATION NUMBER: US 08/459,504			
FILING DATE: 02-JUN-1995			
APPLICATION NUMBER: US 07/951,715			
FILING DATE: 25-SEP-1992			
APPLICATION NUMBER: US 07/772,027			
FILING DATE: 04-OCT-1991			
ATTORNEY/AGENT INFORMATION:			
NAME: Meigs, J. Timothy			
REGISTRATION NUMBER: 38,241			
REFERENCE/DOCKET NUMBER: S-188051			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (919)541-8587			
TELEFAX: (919)541-8689			
INFORMATION FOR SEQ ID NO: 22:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 464 amino acids			
TYPE: amino acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: protein			
HYPOTHETICAL: NO			
FEATURE:			
NAME/KEY: Protein			
LOCATION: 1..464			
OTHER INFORMATION: /note= "derived protein sequence of			
pollen specific CDPK as disclosed in Figure 34."			
SEQUENCE DESCRIPTION: SEQ ID NO: 22:			
US-09-988-462-22			
Query Match 55.4%; Score 1437.5; DB 11; Length 464;			
Best Local Similarity 60.9%; Pred. No. 3.2e-100;			
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;			
QY	22	LRDHYLLGKLGQGGTGYLCTEKTSANYACKSIPEKLVCRDVEDVMEIQIMHHL	81
Db	9	VRATYSGVELGQGGVTHLCTHRTSGEKLACKIAKKLAAREDDVDVREVMHHL	68
QY	82	SEHPNVIRIKGYEDSVFVHIVMEVCEGGELFDRIVSKHFSEBAVKLIKTLGVBEAC	141
Db	69	SGQPNVVGURGAYEDKQSVHLWELCAGGELFDRIIARGQYTERGAELLRAIVQIVHTC	128

	Query Match	55.4%	Score 1437.5;	DB 11;	Length 464;
	Best Local Similarity	60.9%;	Pred. No. 3.2e-100;		
	Matches 271;	Conservative 70;	Mismatches 103;	Indels 1;	Gaps 1
QY	22 LRDHLLGKKGQQGFQGTYYLCTSEKSTSNANVACKSIPIRKLUVCRDEYEDVMREIQIMHHL	81	:	:	:
Dd	: : : : : : : : : :	:	:	:	:
	9 VRATYSMGKELGRCQGFGVTTHLTCHRTSGEKLACCKTIKRKLAREDDVDVRREVQIMHHL	68	:	:	:
QY	82 SEHPNVVRIKGTVEDSYFVHVLMVEVCGGELFDRIIVSKGHSPSERAVNLIKITILGVTEAC	141	:	:	:
Dd	: : : : : : : : :	:	:	:	:
	69 SGQPNVVGLRGAYEDKDSVLHMVELCAGGEFLDRIIARGQYTERGAELLRAIVQIVHTC	128	:	:	:

Qy	5	PNPRPSPNTVLVY-----QTPR-----	21
Db	62	PSPRHPSASPLPHYTSSPAPSTPRNNFKRPFPFSPAKHQSSLVKRHGAKPKCEGAIP	121
Qy	22	-----LRDH-----YLLGKKLGQQFGTGYLYCTSKSTSANY-----ACKSIP	58
Db	122	EAVDGEKPLDRHGFGYHKNFATKYELGHEVGRRGHFGHT--CYAKVRKGEKHGOAVAKIIS	179
Qy	59	KRKLCREDEDVMREIOIMHLBSHPNVRIKGTYESDVFFVIIVMEVCCEGGLFDRIVS	118
Db	180	KAKMTTATAIEDVGREVKILKALTGHQNLVRFYDSCEDHLNVYIWMELCEGGELLDRILS	239
Qy	119	K-GHFSEREAVKLINTLIGVVEACHSLGWHRDLKPENLPDFSPDKDDAKLKATDFGLSVF	177
Db	240	RGGKYSBEDAKVVRQILSVAFCHLQGWHRDLPENLFFTTKDEYAQLKAIDFGLSDF	299
Qy	178	YKPGOYLVDVGVSPYYVAPEVLKCCYGPBIDWWSAGVILYILLSGVPPFWAETESGI	237
Db	300	IKPOERLNDIVGSAYYVAPEVLHRLYSMEADWMSIGVTITYLLCGSRPFWARTESGIFRA	359
Qy	238	ILOGKLDFKSDPWPTISAAXKDLYIKMLERSPKKRISAHAELCPHWIDEQAAPDKPLDP	297
Db	360	VLRADPSEEPWPSSIPEAKDFVKRLNKDMRKMTAAQALTHPIWIRSNV--KIPLDI	417
Qy	298	AVLSRLKFOSOMNIKKQVALRVIAERLSEEIGGLKELFKMIDTNSGTITITEELKAGLX	357
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Qy	358	RVGSELW-ESIKSJMDAADTNSGTIDYGFEFLAATHLNKNOR-----EELIUAFPSDF	412
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Qy	413	KDGSGYITIDELQSACTEFGLC-DTPLD---DMTKEIDLNDGDKIDFSEFTAMMRKGDCV	468
Db	538	KEGNRVYPDEL---AKEMWGLAPNVPAQVFLDWRQ----SDGRLSFTGFTKLLH-----	585
Qy	469	GRSRTMMKNUL	478
Db	586	GISSRAIKNL	595

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RESULT 11
US-09-854-731-4
; Sequence 4, Application US/09854731
; Patent No. US2002120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854.731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-854-731-4
Query Match 32.0%; Score 829; DB 10; Length 623;
Best Local Similarity 40.6%; Pred. No. 3.3e-54;
Matches 18%; Conservative 87; Mismatches 155; Indels 26; Gaps 11;

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Qy	26	YLIGKKLGQCGPGTYYLCTEKSTSNY-----ACKSIPKPKLVCREDYEDVWREIQIMHH	80
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Qy	81	LSBHPNVRIKGYEDSVFVHIVMEVCEGGELEDRIYSK-CHFSEREAVKLIKTLGVVE	139
Db	230	LSGHNNLVKPYDACDGLNYYIWMELCEGGELEDRIILARGGRVTEDAKAIIVVQLSWA	289


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/ GENERAL INFORMATION:
/ APPLICANT: Millennium Pharmaceuticals, Inc
/ APPLICANT: Hunter, John Joseph
/ APPLICANT: MacBeth, Kyle J.
/ APPLICANT: Tsai, Fong-Ying
/ APPLICANT: Lesoon, Andrea
/ APPLICANT: Lightcap, Eric S.
/ APPLICANT: Williamson, Mark
/ APPLICANT: Rudolph-Owen, Laura A.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
/ TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
/ TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
/ TITLE OF INVENTION: 3703, 14171, 10359, 1560, 1450, 18894, 2088, 32427, 2160,
/ TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
/ TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 33230, 1586, 9943,
/ TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
/ FILE REFERENCE: MPI02-020PIRNONMIM
/ CURRENT APPLICATION NUMBER: US/10/354,358
/ CURRENT FILING DATE: 2003-01-30
/ PRIOR APPLICATION NUMBER: US 60/353,600
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 60/364,517
/ PRIOR FILING DATE: 2002-03-15
/ PRIOR APPLICATION NUMBER: US 60/371,075
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: US 60/371,507
/ PRIOR FILING DATE: 2002-04-10
/ PRIOR APPLICATION NUMBER: US 60/372,984
/ PRIOR FILING DATE: 2002-04-16
/ PRIOR APPLICATION NUMBER: US 60/374,194
/ PRIOR FILING DATE: 2002-04-19
/ PRIOR APPLICATION NUMBER: US 60/382,995
/ PRIOR FILING DATE: 2002-05-24
/ PRIOR APPLICATION NUMBER: US 60/385,023
/ PRIOR FILING DATE: 2002-05-31
/ PRIOR APPLICATION NUMBER: US 60/388,853
/ PRIOR FILING DATE: 2002-06-14
/ PRIOR APPLICATION NUMBER: US 60/389,395
/ PRIOR FILING DATE: 2002-06-17
/ Remaining Prior Application data removed - See File wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 122
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 88
/ LENGTH: 499
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-354-358-88

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Query Match		22.8%; Score 591; DB 12; Length 499;
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QY	21	RLEHDHLLGKKGCGFTTYLCTEKSTSNYACKSIPKRKLVCREDYEDVWRIQMHH 80
Ddb	9	RTDEYQLFEELGGKGAFSVVRRCKMPTGQGYAAKIINTKKLSAR-DHQKLEREARIC-R 66
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Ddb	67	LKHKNIVRLHDSISEEGPHYLFDLVTTGGELFEDIIVAREYISEADASHCIQTLESVNH 126
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QY	200	KK-CYGPETDWSAGVILIILSGVPFFWAETESGIFRQILOGKLPDKSPWPTISAAPK 258
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QY	259	DLIIYKMLESPPKRIISAHEALCHPWIVDEQAAPDKPLDPAVL SRLQFOSQMNKIKMALR 318
Ddb	247	DUINKMLTINPAKRITASALKHPWTFCQRSTVASMMHROETVDCLKKFNNARRKLKG---A 303

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Db   304 ILTTMLATRFNFAAKSLKKPKGVKESTESSNTTIEDEDVKARKOEIINKVTEQLIEA--- 360
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RESULT 15
US-09-935-464-36
; Sequence 36, Application US/09935464
; Publication No. US20030027153A1
; GENERAL INFORMATION:
; APPLICANT: Meyer, Joanne
; APPLICANT: Barrington-Martin, Rory
; APPLICANT: Parker, Alexander
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING MEN
; TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
; FILE REFERENCE: 3222/LH702 US1
; CURRENT APPLICATION NUMBER: US/09/935,464
; PRIORITY FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 09/757,300
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 317
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-935-464-16
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Qy	198	VL-KCYGPEDVWSAGVILYILLSGVPFPFAETESGIFRQILOGKLDKFSDPWPTISEA	256						
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Search completed: November 28, 2003, 10:48:56
Job time : 260 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 28, 2003, 10:37:02 ; Search time 5521 Seconds
(without alignments)

3667.862 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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RESULT 1

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2593	100.0	1747	8	ATHCDPKB
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3	2577	99.4	1519	8	AY113986 Arabidops
4	2577	99.4	1750	8	AY050981 Arabidops
5	2458	94.8	1657	8	ATU31752 Arabidops
6	2188	84.4	158096	8	AC007887 Genomic s
7	2087	80.5	197876	8	AL161831 Arabidops
8	2087	80.5	197394	8	AT161515 Arabidops
9	2064	79.6	1473	8	AY247755 Glycine m
10	2030	78.3	1754	8	GMU69173 Glycine m
11	1969.5	76.0	1732	8	AB051809 Solanum t
12	1944	75.0	1768	8	AX077706 Sequence
13	1944	75.0	1768	8	SOYCADPK
14	1937	74.7	1524	8	AY247754 Glycine m
15	1844.5	71.1	1473	6	AX506091 Sequence
16	1844.5	71.1	1693	8	ATACDPK9 Arabidops
17	1779.5	68.6	2126	8	AB042550 Oryza sat
18	1767	68.1	2439	6	AX653934 Sequence
19	1762	68.0	2022	6	AX077717 Sequence
20	1762	68.0	2022	6	VRU08140 Vigna radi
21	1759	67.8	1719	6	AX653531 Sequence
22	1752	67.6	1857	8	D84408 Maize mRNA
23	1746	67.3	2214	8	AY072802 Cucurbita
24	1745	67.3	2248	8	D87042 Zea mays mr
25	1742	67.2	1967	8	ATU31834 Arabidops
26	1739.5	67.1	2393	8	AB051808 Solanum t
27	1738	67.0	2270	8	AY072801 Cucurbita
28	1733.5	66.9	2437	6	NTA344155 Nicotiana
29	1731	66.8	1635	6	AX507649 Sequence
30	1731	66.8	1635	6	AX651703 Sequence
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32	1731	66.8	2036	8	ATU31835 Arabidops
33	1731	66.8	2197	8	AY140007 Arabidops
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35	1724	66.5	1833	6	AX507639 Sequence
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38	1724	66.5	2521	8	AK118706 Arabidops
39	1719	66.3	2142	8	ATU31833 Arabidops
40	1717.5	66.2	2243	8	TRU82087 Arabidops
41	1717	66.2	2185	8	AY295081 Capsicum
42	1709.5	65.9	1858	8	ATHATCDPK Arabidops
43	1709.5	65.9	2550	6	AX077715 Sequence
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ALIGNMENTS

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 accession GI:1235717
 version 1
 keywords calcium-dependent protein kinase; ATCDPK2.
 source Arabidopsis thaliana (chale cress)
 ORGANISM Arabidopsis thaliana
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 Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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 AUTHORS Urao,T., Katagiri,T., Mizoguchi,T., Yamaguchi-Shinozaki,K.,
 Hayashida,N. and Shinozaki,K.
 TITLE Two genes that encode Ca(2+)-dependent protein kinases are induced
 by drought and high-salt stresses in Arabidopsis thaliana
 JOURNAL Mol. Gen. Genet. 244 (4), 331-340 (1994)
 MEDLINE 94359455
 PUBMED 8078458
 REFERENCE 2 (bases 1 to 1747)
 AUTHORS Shinozaki,K.
 TITLE Direct Submission
 JOURNAL Submitted (30-OCT-1993) Kazuo Shinozaki, Tsukuba Life Science
 Center, The Inst. of Physical and Chemical Res.; 3-1-1 Kohyadai,
 Tsukuba, Ibaraki 350, Japan (E-mail:sinozaki@rtcs1.riken.go.jp,
 Tel:0298-36-4359, Fax:0298-36-9060)
 COMMENT On Mar 22, 1996 this sequence version replaced gi:540482.
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 ORIGIN

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 Score: 2593.00 Matches: 495
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

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 Db 127 CGATTAAAGAGATCAATTACCTTCTCGGAAAAAAGTAGCCCAAGCCCAATTTTGGACAAC 186
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 QY 61 LysLeuValCysArgGluAspTyrGluAspValTrpArgGluLeuGlnIleMetHisHis 80
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 QY 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100
 Db 307 CTCTCTGAGCATCCAAATGTTTGTAGGATCAAGGGACTTATGAAGATTCGGTGTGTGT 366
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 Db 367 CATATTGTTATGGAGGTTTGTGAAGTGTGTGAGCTTTTGTATCGATGTTTCTTAAGGT 426
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DEFINITION Sequence 704 from Patent WO0216655.
ACCESSION AX506009
VERSION AX506009.1 GI:23387246
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
REFERENCE
AUTHORS Harper J.F., Kreps, J., Wang, X. and Zhu, T.
TITLE Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
JOURNAL Patent: WO 0216655-A 704 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)
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Best Local Similarity: 99.60% Mismatches: 2
Query Match: 99.38% Indels: 0
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LOCUS AY113986 1519 bp mRNA linear PLN 18-SEP-2002

DEFINITION Arabidopsis thaliana putative calcium-dependent protein kinase

ACCESSION AY113986

VERSION AY113986.1

KEYWORDS GI:21281140

SOURCE FLJ CDNA

ORGANISM Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1519)

Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Arabidopsis Open Reading Frame (ORF) Clones

Unpublished

2 (bases 1 to 1519)

Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Direct Submission

Submitted (16-MAY-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAPL cDNAs: Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers

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Pred. No.: 5,75e-193 Length: 1519

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Percent Similarity: 99.60% Conservative: 0

Best Local Similarity: 99.60% Mismatches: 2

Query Match: 99.38% Indels: 0

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 LOCUS
 DEFINITION Arabidopsis thaliana putative calcium-dependent protein kinase
 1750 bp mRNA linear PLN 18-SEP-2002

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
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 AUTHORS
 TITLE
 JOURNAL
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 JOURNAL
 COMMENT
 FEATURES
 source

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 Goldsmith,A.D., Lee,J.M., Quach,H.D., Toriumi,M., Yu,G., Bowser,L.,
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 Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and
 Theologis,A.
 Direct Submission
 Submitted (07-AUG-2001) Plant Gene Expression Center, 800 Buchanan
 Street, Albany, CA 94710, USA
 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
 Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J.,
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
 Hayashizaki,Y. and Shinozaki,K.
 The Salk, Stanford, PGEC (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X.,
 Pham,P.K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D.,
 Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.D., Tang,C.C.,
 Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H.,
 Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B.,
 Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P.,
 Southwick,A., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A.
 Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to
 this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC)
 contributed equally to this work as PIs.
 Annotation is based on the January 2002 version of the Arabidopsis
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ORGANISM Arabidopsis thaliana
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1 (bases 1 to 158096)
Ecker, J.R.
Direct Submission
Submitted (22-JUN-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA.
2 (bases 1 to 158096)
Ecker, J.R.
Direct Submission
Submitted (04-OCT-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA.
3 (bases 1 to 158096)
Cheuk, R., Shim, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Chlou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.
Direct Submission
Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA
On Jun 28, 2000 this sequence version replaced gi:6007863.
This submission of BAC F1504 is shorter by 1338 bases. The original BAC had a Tn10 transposon insertion (GbJ01829.1|TRN101813) from E. coli located at the junction of bases 18229 and 18230 of this submission.
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Alignment Scores:

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Query Match:	84.38%	Indels:	379
DB:	8	Gaps:	6

US-09-848-806-1 (1-495) x AC007887 (1-158096)

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Qy 211 SerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValProProPheTrpAla----- 228
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Qy 228 ----- 228
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Qy 229 -----GluThrGluSerGlyIlePheArgGlnIleLeuGln 240
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Qy 449 ----- 449
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VERSION AL161831 AC007633
KEYWORDS AL161831.1 GI:7321075
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 97876)
AUTHORS McCombie,R.W., Spiegel,L.A., Huang,E.N., Nascimento,L.U., de la
Bastide,M., Vil,D.M., Preston,R.R., Matero,A., Shah,R.,
O'Shaughnessy,A., Rodriguez,M., Shekher,M., Schurz,K., See,L.H.,
Swaby,I., Habermann,K., Dedhia,N.N., Mewes,H.W., Lemcke,K. and
Mayer,K.F.X.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 97876)
AUTHORS EU Arabidopsis sequencing project.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-2000) MIPS at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de
On Jun 22, 2000 this sequence version replaced gi:5916440.
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
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Best Local Similarity: 53.56% Mismatches: 16
Query Match: 80.49% Indels: 383
DB: 8 Gaps: 7

US-09-848-806-1 (1-495) x ATT25P22 (1-97876)

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Db 20205 TGTCTGAGACTACGAAGATGATGGCTGAGATTTCATGATCATCTCTCTGAG 20264
Qy 84 HisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleVal 103
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	TITLE	Direct Submission
	JOURNAL	Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk
	COMMENT	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/ this fragment has an overlap with ATCHRIV26 at the 5' end and an overlap with ATCHRIV28 at the 3' end.
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DEFINITION
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ACCESSION
AY247755
VERSION
AY247755.1 GI:29892203
KEYWORDS
  Glycine max (soybean)
ORGANISM
  Glycine max
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
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  Glycine.
REFERENCE
  1 (bases 1 to 1473)
  Tang, G.-Q., Dewey, R. and Huber, S.C.
  Biochemical characterization of calcium dependent protein kinase
  from Glycine max
  Unpublished
  2 (bases 1 to 1473)
  Tang, G.-Q., Dewey, R. and Huber, S.C.
  Direct Submission
  Submitted (03-MAR-2003) Agricultural Research Service, US
  Department of Agriculture, 3127 Ligon Street, Raleigh, NC 27607,
  USA
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  Qy 54 CysLysSerIleProLysArgLysLeuValCysArgGluAspTyrGluAspValTyrArg 73
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 mRNA, complete cds.
 U69173

ACCESSION U69173.1 GI:2501763
 VERSION
 KEYWORDS CDPK; calmodulin-like domain protein kinase; calcium-dependent
 protein kinase.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.

REFERENCE 1 (bases 1 to 1754)
 AUTHORS Lee,J.-Y., Roberts,D.M. and Harmon,A.C.
 TITLE Isolation of two new CDPK isoforms (Accession Nos. U69173 and
 JOURNAL U69174) from soybean (Glycine max L.) (PGR97-128)
 REFERENCE 2 (bases 1 to 1754)
 AUTHORS Lee,J.-Y., Yoo,B.-C. and Harmon,A.C.
 TITLE Direct Submission

JOURNAL Submitted (03-SEP-1996) Botany, University of Florida, 220, Bartram
 Hall, P.O. Box 119526, Gainesville, FL 32611, USA

FEATURES
 Location/Qualifiers
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VERSION
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ORGANISM Solanum tuberosum
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1 Furuichi,N., Okuta,T. and Hara,N.
Calcium dependent protein kinase genes from resistant and susceptible potato cultivars to Phytophthora infestans
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1732)
AUTHORS Furuichi,N. and Okuta,T.
TITLE Direct Submission
JOURNAL Submitted (25-NOV-2000) Naotaka Furuichi, niigata university, Agriculture; 2-8050, Igarashi, Niigata shi, Niigata Ken 950-2181, Japan (E-mail:nfuru@agr.niigata-u.ac.jp, URL:http://www.niigata-u.ac.jp, Tel:81-25-262-7520(ex.7520), Fax:81-25-262-7520)
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ACCESSION   AX077706
VERSION     AX077706.1   GI:13122081
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REFERENCE   1
AUTHORS    Holt,C.D., White,A.J., Michael,A.J. and Osborn,R.W.
TITLE      Herbicide resistant plants and methods for the production thereof
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US-09-848-806-1 (1-495) x AX077706 (1-1768)

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 VERSION M64987.1 GI:169930
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 Charbonneau, H. and Harmon, A.C.
 TITLE A calcium-dependent protein kinase with a regulatory domain similar
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 JOURNAL Science 252 (5008), 951-954 (1991)
 MEDLINE 91240279
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 Score: 1944.00 Matches: 370
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 Best Local Similarity: 77.73% Mismatches: 51
 Query Match: 74.97% Indels: 4
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VERSION
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Glycine max (soybean)
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Glycine max
ORGANISM
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Glycine.
REFERENCE
1 (bases 1 to 1524)
Tang, G.-Q., Dewey, R. and Huber, S.C.
Biochemical characterization of calcium dependent protein kinase
from Glycine max
Unpublished
JOURNAL
2 (bases 1 to 1524)
Tang, G.-Q., Dewey, R. and Huber, S.C.
Direct Submission
AUTHORS
Submitted (03-MAR-2003) Agricultural Research Service, US
JOURNAL
Department of Agriculture, 3127 Ligon Street, Raleigh, NC 27607,
USA
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US-09-848-806-1 (1-495) x AY247754 (1-1524)
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DEFINITION AX506091
ACCESSION AX506091
VERSION AX506091.1 GI:23387328
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
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REFERENCE
AUTHORS Harper, J.F., Krens, J., Wang, X. and Zhu, T.
TITLE Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
JOURNAL Patent: WO 0216655-A 786 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)
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Search completed: November 28, 2003, 12:31:55

Job time : 5723 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 28, 2003, 10:36:27 ; Search time 438 Seconds
(without alignments)
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Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

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1	2593	100.0	1747	24	ABA06021	Arabidopsis CDPK2
2	2577	99.4	1488	24	AB212899	Arabidopsis thalia
3	2458	94.8	1506	21	AAC44687	Arabidopsis thalia
4	2458	94.8	1657	24	ABA06022	Arabidopsis CDPK4
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6	1844.5	71.1	1473	24	AB212981	Vigna radiata calc
7	1762	68.0	2022	22	AAF74285	Arabidopsis thalia
8	1742	67.2	1671	21	AAC42924	Arabidopsis thalia
9	1731	66.8	1635	24	AB214539	Arabidopsis thalia
10	1724	66.5	1833	24	AB214529	Arabidopsis thalia
11	1709.5	65.9	2550	22	AAF74283	Cucurbita pepo cal
12	1703	65.7	3054	21	AAC45753	Arabidopsis thalia
13	1586	61.2	2334	22	AAF74277	Rice calcium depen
14	1531.5	59.1	1647	22	AAF74281	Liverwort calcium
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17	1501	57.9	1332	21	AAC48741	Arabidopsis thalia
18	1484.5	57.3	2251	22	AAF74276	Tobacco calcium de
19	1482	57.2	2040	22	AAF74278	Rice calcium depen
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21	1462	56.4	1761	21	AAC42353	Arabidopsis thalia
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24	1457	56.2	2466	15	AAQ66397	Protein kinase cDN
25	1455	56.1	2363	22	AAF74284	Common ice plant c
26	1432.5	55.2	1791	22	AAF74270	Carrot calcium dep
27	1431	55.2	1910	22	AAF74275	Sweet potato calci
28	1381	53.3	1638	22	AB214054	Arabidopsis thalia
29	1336	51.5	1967	22	AB214280	Strawberry calcium
30	1325.5	51.1	1836	21	AAC47633	Arabidopsis thalia
31	1313.5	50.7	1602	24	AB214499	Arabidopsis thalia
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36	1134	43.7	1082138	21	AAF22305	Tobacco CDPK cDNA.
37	1091	42.1	13114	21	AAA60744	Arabidopsis thalia
38	1049.5	40.5	1133	22	AAC85833	Rice gene for resi
39	1019.5	39.3	1781	21	AAC34898	Tobacco homolog of
40	985.5	38.0	2210	22	AAF74279	Arabidopsis thalia
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ALIGNMENTS

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AC ABA06021;
XX
XX
DT 08-MAR-2002 (first entry)
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XX Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed;
XX disease resistance; agricultural; pathogen; crop yield; ornamental;
XX fungicide; bactericide; nematocide; insecticide; viricide; cereal;
XX transgenic; plant; enzyme; gene; 5s.
XX Arabidopsis thaliana.
OS
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FH Key Location/Qualifiers
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 XX 15-NOV-2001.
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 XX 04-MAY-2001; 2001WO-US14368.
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 XX 05-MAY-2000; 2000US-201925P.
 PR
 XX (GEHO) GEN HOSPITAL CORP.
 XX
 XX Sheen J;
 PI
 XX WPI; 2002-062179/08.
 DR P-PSDB; AAM48000.
 DR
 XX
 XX Producing plant having increased disease resistance, comprises
 PT regenerating plant from a non-naturally occurring plant cell
 PT over-expressing a polynucleotide encoding a calcium dependent protein
 PT kinase polypeptide -
 XX
 XX Disclosure; Fig 1; 44pp; English.
 PS
 PS
 XX
 CC The invention relates to producing a plant having increased disease
 CC resistance, comprising providing a non-naturally occurring plant cell
 CC over-expressing a polynucleotide encoding a calcium dependent protein
 CC kinase (CDPK) polypeptide and regenerating a plant from the plant
 CC cell, where the CDPK polypeptide is expressed in the plant, increasing
 CC the resistance of the plant to disease as compared to a
 CC naturally-occurring plant. The method is useful for a variety of
 CC agricultural and commercial purposes, including improving a plant's
 CC resistance against plant pathogens, increasing crop yields, improving
 CC crop and ornamental quality and reducing agricultural production costs.
 CC The method facilitates an effective and economical method for in-plant
 CC protection against plant pathogen, reducing or minimising the need for
 CC traditional chemical practices (e.g. application of fungicides,
 CC bactericides, nematocides, insecticides or viciides) that are typically
 CC used by farmers for controlling the spread of plant pathogens and
 CC providing protection against disease causing pathogens. The method
 CC contributes to the production of high quality and high yield agricultural
 CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops
 CC having reduced spots, blemishes and blotches that are caused by
 CC pathogens, agricultural products with increased shelf-life and reduced
 CC handling costs and high quality and yield crops for agricultural
 CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial
 CC (e.g. fiber crops) purposes. The present sequence is that of Abrabidopsis
 CC thaliana CDPK2 of the invention.
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 SQ Sequence 1747 BP; 516 A; 316 C; 392 G; 523 T; 0 other;

Alignment Scores:
 Pred. No.: 2,36e-245 Length: 1747
 Score: 2593.00 Matches: 495
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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US-09-848-806-1 (1-495) x ABA06021 (1-1747)

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Qy 481 AsnIleLeuAspAlaPheGlyValAspGlyGluLysSerAspAsp 495
Db 1507 AACATTGCTGATGCTTTTGGAGTTGATGGTCAAAAAATCTGATGAC 1551

RESULT 2

ABZ12899
ID ABZ12899 standard; DNA; 1498 BP.

XX ABZ12899;

AC AC
XX XX
DT 21-JAN-2003 (first entry)

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 704.

DE Arabidopsis thaliana; plant; gene; stress; transgenic; da.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX WO200216655-A2.

PN 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US26685.

XX 24-AUG-2000; 2000US-227866P.

PR 26-JAN-2001; 2001US-264647P.

XX 22-JUN-2001; 2001US-300111P.

XX (SCRI) SCRIPPS RES INST.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

PI WPI; 2002-304127/34.

XX Identifying a stress condition to which a plant cell has been exposed

PT and producing plants with increased tolerance to these abiotic stresses

PT -

XX Claim 144; SEQ ID NO 704; 577pp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant

CC cell has been exposed, comprising:

CC (a) contacting nucleic acid representative of expressed polynucleotides

CC in the plant cell with an array or probes representative of the plant

CC cell genome; and

CC (b) detecting a profile of expressed polynucleotides in the plant cell

CC characteristic of a stress response. The method is useful in the

CC production of transgenic plants, cells and seeds and in producing plants

CC with increased tolerance to abiotic stress. The present sequence is that

CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used

CC in methods of the invention.

CC Note: The sequence data for this patent is not represented in the printed

CC specification but is based on sequence information supplied to Derwent by

CC the European Patent Office.

XX SQ Sequence 1498 BP; 443 A; 271 C; 365 G; 409 T; 0 other;

XX Alignment Scores:

Pred. No.: 7.16e-244 Length: 1488
Score: 2577.00 Matches: 493
Percent Similarity: 99.60% Conservative: 0
Best Local Similarity: 99.60% Mismatches: 2
Query Match: 99.38% Indels: 0
DB: 24 Gaps: 0

US-09-848-806-1 (1-495) x ABZ12899 (1-1498)

Qy 1 MetGluThrLysProAsnProArgProSerAsnThrValLeuProTyGlnThrPro 20

Db 1 ATGGAGACGAGCCAAACCCCTAGACGCTCTTCAAACACAGTTCTACCATATCAAAACCA 60

Qy 21 ArgLeuArgAspHisTyLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThr 40

Db 61 CGATTAAGATGATCATTACCTTCTGGGAAAAAANGCTAGCCCAAGGCCAATTTGGAAACA 120

Qy 41 TyrLeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArg 60

Db 121 TATCTCTGCACAGAGAAATCAACCTCGCTAAATACGCTGCAAAATCGATCCCGAAGCGA 180

Qy 61 LysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMetHisHis 80

Db 181 AAGCTCGTGTGTCGCGAGGATTCGAAAGATGTATGGCGTGAGATTCAGATCATCATCAT 240

Qy 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100

Db 241 CTCTCTGAGCATCAAAATGTTGTAGGATCAAGGGACTTATGAAGATTCGGTGTGGT 300

Qy 101 HisIleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGly 120

Db 301 CATATTGTTATGGAGGTTTGTGAAGTGGTGAGCTTTTGTGATCGGATTTGTTCTAAAG 360

Qy 121 HisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAla 140

Db 361 CATTTTAAAGTGAAGCTGAAAGCTGTCACAGCTTATTAAGACGATTCCTGGTGTGG 420

Qy 141 CysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSer 160

Db 421 TGTCAATCTCTTGGTGTATGATGATAGATCTCAACCTGAGAAATTTCTGTTGTGATAG 480

Qy 161 ProllysAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyLysPro 180

Db 481 CCTAAAGATGATGCTAAGCTTAAGGCTACCGATTTTGGTGTGTCTCTCTATAAGCCA 540

Qy 181 GlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLys 200

Db 541 GGACAATATTATATGACGTAGTGGAAAGTCCGCTACTATGTGTCACAGAGGTCCTAAAG 600

Qy 201 LysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu 220

Db 601 AAATGTTATGACCTGAAATAGATGTGTGGAGTGTGGTGTATCTCTCTACATTTTACTC 660

Qy 221 SerGlyValProPheThrAlaGluThrGluSerGlyIlePheArgGlnIleLeuGln 240

Db 661 AGCGGTGTCTCTCCCTCTCGGCAGACACTGAGTCTGGAATCTTTAGACAGATATGCA 720

Qy 241 GlyLysLeuAspPheLysSerAspProTyrProThrIleSerGluAlaAlaLysAspLeu 260

Db 721 GGGAAAGTTAGATTCAAAATCTGACCCGTGGCTACTATCTCAGAAGCTGCTAAAGATT 780

Qy 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCys 280

Db 781 ATCTATAAAATGCTCGAAGAGGAGCCCCCAAGAAACGCATTTCTGCTCATGAAGCCCT 840

Qy 281 HisProTrpIleValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeu 300

Db 841 CACCCATGGATTTCGATGAACAAGCAGCACCAGCAAGCCCTCTTGTATGACGAGCTCT 900

Qy 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIle 320

Db 901 TCTCGTCTAAAGCAGTTTTTCTCAAAATGAATGAATTAAGAAATTAAGCAATTTACGG 960

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OY 321 AlaGluArgLeuSerGluGluGluLeuGlyGlyLeuLysGluLeuPheLysMetIleAsp 340
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OY 341 ThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGly 360
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OY 361 SerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSer 380
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Db 1081 TCTGAACATGATGGAATCAGAAATCAAGTCTCTCATGGATCGCGCTGATATCGACAACAGT 1140
OY 381 GlyThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArg 400
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Db 1141 GGTACAATAGACTACGGAGAATTCCTAGCAGCAACCTTACACATGACAAGATGGAGAGA 1200
OY 401 GluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThr 420
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Db 1201 GAGGAGAATCTGGTGGCTGCAATTTTCGTACTTTGACAAAGACGGAAGCGGTTATATCACC 1260
OY 421 IleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAsp 440
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Db 1261 ATCGATGAGCTTCAGTCAGCTTGACAGAGTTTGGTCTATGTGATACACCTCTGGACCAC 1320
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Db 1321 ATGATCAAGGAGATTGATCTTGACAAATGACGGGAAGATCGATTTCCTCGGAGTTTACAGCA 1380
OY 461 MetMetArgLysGlyAspGlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPhe 480
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Db 1381 ATGATGAGGAAGGAGATGGAGTTGGGAGAGCAGACCAATCATGATGAAGAACTTGAACCTTC 1440
OY 481 AsnIleAlaAspAlaPheGlyValAspGlyGluLysSerAspAsp 495
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RESULT 3
AAC44687
ID AAC44687 standard; DNA; 1506 BP.
AC AAC44687;
XX
XX 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 43752.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
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XX 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
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PR 07-SEP-1999; 99US-0152363.
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PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 18-OCT-1999; 99US-0159584.

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Alignment Scores:
Pred. No.: 3,78e-232 Length: 1506
Score: 2458.00 Matches: 470
Percent Similarity: 96.57% Conservative: 9
Best Local Similarity: 94.76% Mismatches: 13
Query Match: 94.79% Indels: 4
DB: 21 Gaps: 1

US-09-848-806-1 (1-495) x AAC44687 (1-1506)

QY 4 LysProAsnProArgArgProSerAsnThrValLeuProTyrGlnThrProArgLeuArg 23
Db 7 AAACCAACCCCTAGAAAGACCCCTCAAAACAGTGTCTTCCATACGAACACCAAGATTAAAG 66
QY 24 AspHisTyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnGlyThrThrThrTyrLeuCys 43
Db 67 GATCACTATCTCTCGGCAAAAGCTAGGCCAAGGCCAAATTTGGAAACCAACTATCTCTGT 126
QY 44 ThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuVal 63
Db 127 ACAGAGAAATCATCATCATGCTTAATACGCTTGCAATCAATCCAAACGTAAGCTTGTGA 186
QY 64 CysArgGluAspTyrGluAspValTrpArgGluLleGlnIleMetHisHisLeuSerGlu 83
Db 187 TGTGCTGAAGACTACGAAGATGTATGGCGTGAGATTTCAGATCATCATCATCTCTGAG 246
QY 84 HisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleVal 103
Db 247 CATCCTAATGTGTAGAAATCAAGGGTACTTATGAAGACTCTCTGTTTTTGTTCACATTGT 306
QY 104 MetGluValCysGluGlyGluLeuPheAspArgIleValSerLysGlyHisPheSer 123
Db 307 ATGGAAGTTTGTGAAGTGGTGAGCTTTTTCATCGGATGTCTTAAAGGGGTGTTTGTAGT 366
QY 124 GluArgGluAlaValLysLeuLysThrIleLeuGlyValValGluAlaCysHisSer 143
Db 367 GAACGTGAAGCTGCTAAGTTTCATTAAAGACTATTCTGTGTGTGTGTGAGGCTTGTCATTCT 426
QY 144 LeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAsp 163
Db 427 CTTGGTGTATGTCATAGAGATCTTAAAGCCTGAGAAATTTCTTGTGTGTGTAGTCCAGTGAT 486
QY 164 AspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyr 183
Db 487 GATGCTAAGCTTAAAGCTACAGACTTTGGTTTGTCTTCTTCTCAAGCCAGGGCAGTAT 546
QY 184 LeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyr 203
Db 547 CTGTATGATGTAGTTGGAAGTCCGCTATTATGTTGCACCTGAGGTTCTGAAAGAAATGTTAT 606
QY 204 GlyProGluLleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyVal 223
Db 607 GGACCAGAGATAGACGTGTGGAGCCGGTGTATCTTGTATACATCTTACTAAGTGGGGTT 666
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Qy	44	ThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuVal	63
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Qy	64	CysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMetHisHisLeuSerGlu	83
Db	187	TGTCGTGAAGACTCAGCAAGATGTATGGCGTGAGATTTCAGATCATCATCTCTCTCTGAG	246
Qy	84	HisProAsnValAlaArgIleLysGlyThrTyrGluAspSerValPheValHisIleVal	103
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Qy	104	MetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSer	123
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Qy	124	GluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSer	143
Db	367	GAACTGTGAAGCTGCTTAAGTTGATTAAGACTATTCTTGGTGTGTTGTGAGCGTTGTCATTCT	426
Qy	144	LeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAsp	163
Db	427	CTTGTGTTATCATAGAGATCTTAAGCCCTGAGAATTTCTTGTTTGATAGTCCCAAGTCAT	486
Qy	164	AspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyr	183
Db	487	GATGCTAAGCTTAAAGCTACAGACTTTGGTTTGTCTGCTCTTACAAGCCAGGGCAGTAT	546
Qy	184	LeuTyrAspValAlaGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyr	203
Db	547	CTGTATGATGTTGGGAAGTCGGTATTATGTTGCACCTGAGGTTCTCAAGAAATGTTAT	606
Qy	204	GlyProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyVal	223
Db	607	GGACCAGAGATAGACGTGTGGAGCCGGTGTTATCTTGTACATCTTACTAAGTGGGGTT	666
Qy	224	ProProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeu	243
Db	667	CCTCCTTTTGGGCAGAAACCGAGTCAGGAATCTTTTAGCCAGATATTCAAGGGGAAGATA	726
Qy	244	AspPheLysSerAspProTrpProThrIleSerGluAlaAlaLysAspLeuIleTyrLys	263
Db	727	GATTTTAAATCTGATCCGTGGCCTACTTCTCAGAAGGTGCTAAAGATTGTGATTACAAA	786
Qy	264	MetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCysHisProTrp	283
Db	787	ATGCTCGATAGAGCCCCAAGAAACGTATTTCTGCACATGAAGCATTTGTCTACCCCTTGG	846
Qy	284	IleValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeu	303
Db	847	ATTGTTGATGAAATCATGCTGCACACAGAACGGCTCTCGACCCAGCAGTCTTCTCGCAGCTT	906
Qy	304	LysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAlaGluArg	323
Db	907	AAGCAGTTCTCGCAATCGAATAAATCAAGAAATGGCCTTTACCAGTAAATCGCGAGAGA	966
Qy	324	LeuSerGluGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAspThrAspAsn	343
Db	967	CTCTCGGAGGAAGAGATTGGTGGTCTGAAGGAAATTTGTTCAAAATCATAGATACAGACAC	1026
Qy	344	SerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGlySerGluLeu	363
Db	1027	AGTCGAACAATCACCTTTGAAGAGCTTAAACAGCGTCTTAAAGAGAGATTGGAATCTGAA	1086
Qy	364	MetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGlyThrIle	383
Db	1087	ATGGAAATCAGAAATCAAGTCTCTTATGGATCGCGCGGATATAGACAAACAGTGGGACAA	1146
Qy	384	AspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArgGluGluIle	403
Db	1147	GACTACGCTGAATTCCTAGCAGCGACATTACATATAACAAGATGGAGAGAGACAGAAC	1206
Qy	404	LeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThrIleAspGlu	423

Db	1207	TTGGTGGTGGCGTTTCATACCTTTGATAAAGATGGTACGGCTTATATACCACTTGACGAG	1266
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QY	464	LysGlyAspGlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPheAsnIleAla	483
Db	1387	AAAGAGAGATGGTGTGGGAGGAGCAGAACTATGAGGAACAACCTTGAACCTTCAATATAGCT	1446
QY	484	AspAlaPheGlyValAspGly-----GluLysSerAspAsp	495
Db	1447	GAAGCTTTTGGAGTTGAGGACACAAAGCAGCACTGCTAAATCTGATGAT	1494
RESULT 5			
AA	AAF74274		
ID	AAF74274	standard; DNA; 1768 BP.	
XX	AAF74274;		
AC	AAF74274;		
XX			
DT	04-MAY-2001	(first entry)	
XX			
DE	Soybean calcium dependent protein kinase clone #2.		
XX			
KW	Calcium dependent protein kinase; CDPK; herbicide resistance;		
KW	paraquat; diquat; crop production; ds.		
XX			
OS	Glycine max.		
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PN	WO200107592-A2.		
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PD	01-FEB-2001.		
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PF	26-JUL-2000; 2000WO-GB02876.		
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PR	27-JUL-1999; 99GB-0017642.		
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PA	(ZENE) ZENECA LTD.		
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PI	Holt CD, White AJ, Michael AJ, Osborn RW;		
XX			
DR	WPI; 2001-168549/17.		
XX			
PT	Producing herbicide resistance plants by inhibiting calcium dependent		
PT	protein kinase in plants or by providing an intracellular vacuolar		
PT	transporter capable of transporting agrochemical into plant vacuole		
XX			
PS	Claim 18; Page 37; 50pp; English.		
XX			
CC	The present invention describes a method of producing plants which are		
CC	resistant to the herbicides paraquat and diquat, involving inhibiting in		
CC	the plants a calcium dependent protein kinase (CDPK) and selecting those		
CC	plants which are resistant to the agrochemical of interest. This is		
CC	useful in the production of crops with herbicide resistance.		
XX			
SQ	Sequence 1768 BP; 511 A; 325 C; 464 G; 468 T; 0 other;		
Alignment Scores:			
Pred. No.:	1.89e-181	Length:	1768
Score:	1944.00	Matches:	370
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Best Local Similarity:	77.73%	Mismatches:	51
Query Match:	74.97%	Indels:	4
DB:	22	Gaps:	3
US-09-848-806-1 (1-495) x AAF74274 (1-1768)			
QY	14	ValLeuProTyrGlnThrProArgLeuArgAspHisTyrLeuGlyValMetLeuGly	23

Db 195 GTTCTCCGCGACGCGACGAGAAATCCGTCAGGTGTACGAGGTTGGCGGAAAGCTCGG 254
Qy 34 GlnGlyGlnPheGlyThrThrTyLeuCysThrGluLysSerThrSerAlaAsnTyAla 53
Db 255 CAGGGCAATTCGGGACCACTTCGAGTGCACGCGCGCTGCGAGTGTGGAAAGTTCGCG 314
Qy 54 CysLysSerIleProLysArgLysLeuValCysArgGluAspTyrGluAspValTyrArg 73
Db 315 TGCAAGTCGATCCGAGCGGAAGCTGCTGTGCAAGGAGGACTACGAGGACGTGTGGCG 374
Qy 74 GluIleGlnIleMetHisHisLeuSerGluHisProAsnValValArgIleLysGlyThr 93
Db 375 GAGATTTCAGATAATGCACCACTTCGCGAACAACGCAACGCTGTGTCGCGCATCGAAGGACG 434
Qy 94 TyrGluAspSerValPheValHisLeuValMetGluValCysGluGlyGlyGluLeuPhe 113
Db 435 TACGAGGATTCACGCGCGTGCACCTGTCATGAGATTGTGCGAGGTTGGAGAGTTGTT 494
Qy 114 AspArgIleValSerLysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThr 133
Db 495 GACAGGATCGTCAGAGGACACTACAGCGAGAGACGCGCGCGGCTTGATAAGACG 554
Qy 134 IleLeuGlyValValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysPro 153
Db 555 ATTCTTGAGGTTGTGAGCGGTGTCACTCGTAGGGGTCAATGATGAGGACCTTAAGCCT 614
Qy 154 GluAsnPheLeuPheAspSerProLysAspAlaLysLeuLysAlaThrAspPheGly 173
Db 615 GAGAAATTCCTGTTGATACCATGATGAGGATGCTAAGCTTAAGGCCACCGATTTCGCG 674
Qy 174 LeuSerValPheTyLysProGlyGlnTyLeuTyAspValValGlySerProTyTyr 193
Db 675 TTGCTCTGTTTTACAAGCTGTTGAATCCTTTGTGATGTTGCGGAGCCCATCAT 734
Qy 194 ValAlaProGluValLeuLysLysCysTyLeuProGluLysAspValTrpSerAlaGly 213
Db 735 GTCCACACAGAGGCTTCGCGCAAGCTCTATGAGCCTGAATCAGATGTTGGAGTGCAGG 794
Qy 214 ValIleLeuTyLysLeuLeuSerGlyValProProPheTrpAlaGluThrGluSerGly 233
Db 795 GTTATTCTGTACATCTTATTAAAGTGGGTGCCACCATTTGGCGCGAATCTGAACCGGG 854
Qy 234 IlePheArgGlnIleLeuGlnGlyLysLeuAspPheLysSerAspProTrpProThrIle 253
Db 855 ATCTTCGACAGATTTTACTAGGAAACTTGATTTTCACTTGAGCCTTGCCCTAGCAT 914
Qy 254 SerGluAlaAlaLysAspLeuIleTyLysMetLeuGluArgSerProLysLysArgIle 273
Db 915 TCAGACAGTGCAGGATCTAAATTCGGAATGCTTGATCAAAATCCAAAACCAAGGCTT 974
Qy 274 SerAlaHisGluAlaLeuCysHisProTrpIleValAspGluGlnAlaAlaProAspLys 293
Db 975 ACAGCATAGTACTCCGCCCATGATGTTGATGACACATGTCACCTGATATAA 1034
Qy 294 ProLeuAspProAlaValLeuSerArgLysGlnPheSerGlnMetAsnLysIleLys 313
Db 1035 CCTCTTGATTCGAGTTTATCAGCTCTGAAACAAATCTCTGCCATGAATAAATGAAA 1094
Qy 314 LysMetAlaLeuArgValIleAlaGluArgLeuSerGluGluIleGlyLeuLys 333
Db 1095 AAGATGCATTCGCTGTTATTCGTGAGAGGCTATCTGAAGAAGAAATGTTGGTACATGAAA 1154
Qy 334 GluLeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLys 353
Db 1155 GAGTTATTCAAGATGATTGACACAGACAAACAGTGGAAACCAATACGTTTGATGATATAA 1214
Qy 354 AlaGlyLeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAsp 373
Db 1215 GATGGTTGAAGCGAGTAGATCTGAACCTTATCGAGTCTGAATCAAGGATCTTATGAT 1274
Qy 374 AlaAlaAspIleAspAsnSerGlyThrIleAspTyLeuGluPheLeuAlaAlaThrLeu 393
|||||

Db 1275 GCTCGGATATTGATAAAGTGGACAAATTGATTATGGTGAATTCATTGCTGCCACTGTT 1334
Qy 394 HisMetAsnLysMetGluArgGluGluIleLeuValAlaAlaPheSerAspPheAspLys 413
Db 1335 CATTTAAATAAGCTGGAGAGAGAAACCTAGTGTGCGCCTTCTCCTATTTTGACAAA 1394
Qy 414 AspGlySerGlyTyIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeu 433
Db 1395 GATGGCAGTGGTTACATAACCTTGTGATGATACACAAAGCTTGTAGGACTTTTGTTTA 1454
Qy 434 CysAspThrProLeuAspAspMetIleLysGluIleAspLeuAspAsnAspGlyLysIle 453
Db 1455 GATGATATCCATATTGACGACATGATCAAGGAATTCATCAAGATAACGATGGCAATA 1514
Qy 454 AspPheSerGluPheThrAlaMetMetArgLysGlyAsp---GlyValGlyArgSerArg 472
Db 1515 GATTATGGGAAATTTGCTGCCATGATGAGAAAGGCAATGGAGGAATTGGAAG---CGA 1571
Qy 473 ThrMetMetLysAsnLeuAsnPheAsnIleAlaAspAlaPheGlyVal 488
Db 1572 ACTATGAGAAAACACTA-----AATTTAAGATGCTCTTGATTA 1613
RESULT 6
ABZ12981
ID ABZ12981 standard; DNA; 1473 BP.
AC ABZ12981;
XX 21-JAN-2003 (first entry)
DT Arabidopsis thaliana stress regulated gene SEQ ID NO 786.
DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
KW Arabidopsis thaliana.
XX Arabidopsis thaliana.
OS WO200216655-A2.
PN 28-FEB-2002.
PD 24-AUG-2001; 2001WO-US26685.
PF 24-AUG-2000; 2000US-227866P.
PR 26-JUN-2001; 2001US-264647P.
PR 22-JUN-2001; 2001US-300111P.
XX (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Harper JF, Kreps J, Wang X, Zhu T;
XX WPI; 2002-304127/34.
XX Identifying a stress condition to which a plant cell has been exposed
and producing plants with increased tolerance to these abiotic stresses
Claim 144; SEQ ID NO 786; 577pp + Sequence Listing; English.
XX The invention relates to identifying a stress condition to which a plant
cell has been exposed, comprising:
CC (a) contacting nucleic acid representative of expressed polynucleotides
in the plant cell with an array or probes representative of the plant
cell genome; and
CC (b) detecting a profile of expressed polynucleotides in the plant cell
characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
in methods of the invention.
CC Note: The sequence data for this patent is not represented in the printed
CC specification but is based on sequence information supplied to Derwent by
CC the European Patent Office.

XX SQ Sequence 1473 BP; 438 A; 257 C; 365 G; 413 T; 0 other;

Alignment Scores:

Pred. No.: 9,22e-172 Length: 1473
 Score: 1844.50 Matches: 353
 Percent Similarity: 84.47% Conservativity: 55
 Best Local Similarity: 73.08% Mismatches: 68
 Query Match: 71.13% Indels: 7
 DB: 24 Gaps: 2

US-09-848-806-1 (1-495) x ABZ12981 (1-1473)

QY 1 MetGluThrLysProAsnProArgArgProSerAsnThrValLeuProTyrGlnThrPro 20
 DB 1 ATGGGCAACAAACAGAACAGAG-----TGGGTTCCTTCTTCAAGACCAAA 48
 QY 21 ArgLeuArgAspHisTyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThr 40
 DB 49 AACGTTGAAGACAACTACTTCTTGGTCAAGTCTTGGACAGGCCAATTCGGNACCCT 108
 QY 41 TyrLeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArg 60
 DB 109 TTCTCTGTATACCAACAGACAGAGGTCAAAAGCTTCCTGCAAAATCCATACCAAAAGG 168
 QY 61 LysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMetHisHis 80
 DB 169 AAGCTCTTGTCAAGAAAGATTACGACGCTTCTGAGAGAGATCCAGATAATGCAATCAC 228
 QY 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100
 DB 229 TTGCTGAATACCCCAACGTTGTCGTATAGAGAGTGGTACGAGGACCAAAACGCTG 288
 QY 101 HisIleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGly 120
 DB 289 CATCTCTGTGATGAGCTTGTGAAGGAGGTGAGTGTGATAGAAATGTTGAAGAGAGGT 348
 QY 121 HisPheSerGluArgGluAlaValLysLeuLysThrIleLeuGlyValValGluAla 140
 DB 349 CATTACAGTGAAGAGAGCTGCTAAGCTTATCAAGACCAATTTGGGGTGTGAGGCG 408
 QY 141 CysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSer 160
 DB 409 TGTCACTCTCTGTTGTTTCATAGAGATCTTAAGCCTGAGAAATTTCTGTTTCTTCT 468
 QY 161 ProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysPro 180
 DB 469 TCTGATGAAGATGCTCTCTTAAATCTACTGACTTTGGCCTCTCTGTTTCTGCACACA 528
 QY 181 GlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLys 200
 DB 529 GGAGAGCATTTTCGGAACCTGTTGGTAGTGCTTACTATGTGGCACCCTGAGGTTTACAT 588
 QY 201 LysCysTyrGlyProGluLeuAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu 220
 DB 589 AAGCATTTATGGTCTCTGAATGTGACGTATGAGTGTGGAGTTATCTCTACATCTCTTA 648
 QY 221 SerGlyValProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGln 240
 DB 649 TGTGGTTCCTCTTTTGGGCTGAGAGTGAATAAGGCATCTTCAAGGAAGATTTTACAG 708
 QY 241 GlyLysLeuAspPheLysSerAspProTyrProThrIleSerGluAlaLysAspLeu 260
 DB 709 GGAAGATGAGTTTGAGATCAATCTTGGCCCTAGCATTTTCAGAGAGTCCCAAGATCTT 768
 QY 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCys 280
 DB 769 ATAAAGAAATGCTTGAAGACATCTTAAAGAGAGCTAACTGCTCATCAAGTGTGTGT 828
 QY 281 HisProTyrIleValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeu 300
 DB 829 CATCCGTGATGTGATGATAAGGTGCTCCAGATAAACCTTTGGACTGCGCGGTAGTG 888

QY 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIle 320
 DB 889 TCCCGCTGAAGAAGTCTCTGCAATGACAACTTAAGAAGATGGCTTTACGAGTTATT 948
 QY 321 AlaGluArgLeuSerGluGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAsp 340
 DB 949 GCAGAGAGACTATCTGAGGAAGAAATCGGTGGTCTCAAGAACTGTTTCAAAATGATAGAC 1008
 QY 341 ThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGly 360
 DB 1009 ACAGATAAAAGTGGGACTATCACGTTTGAAGAGTTAAAGATAGTAGACACGTGTTGGG 1068
 QY 361 SerGluLeuMetGluSerGluLysSerLeuMetAspAlaAlaAspIleAspAsnSer 380
 DB 1069 TCAGAGCTTATGAATCAGAGATCCAAGAACTCTTGGCTGCGGCTGATGTTGATGAGAGT 1128
 QY 381 GlyThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArg 400
 DB 1129 GGAACAAATTGACTATGAGAGTCTTAGCTGCAACCAATCCACTTGAACAAAGCTGGAGAGA 1188
 QY 401 GluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThr 420
 DB 1189 GAGGAGAATCTAGTAGCTGCAATCTCTTCTTTGATAAGGATCCAAAGTGGTTACATCACT 1248
 QY 421 IleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAsp 440
 DB 1249 ATCGAAGAGCTTCAACAGGCAATGGAAGAGTGGTGGTATAAACGATTTCTAATCTTGATGA 1308
 QY 441 MetIleLysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAla 460
 DB 1309 ATGATCAAGAGCAATTCATCAAGATAATGATGGCAAAATAGACTATGGAGAAATTTGTGGCA 1368
 QY 461 MetMetArgLysGlyAspGlyValGlyArgSer-----ArgThrMetMetLysAsn 477
 DB 1369 ATGATCAGGAAGAAATGGCACTGGAGGAGGATTTGGTCCGGAAGAACTATGAGAACTCT 1428
 QY 478 LeuAsnPhe 480
 DB 1429 CTCAACTTT 1437
 RESULT 7
 ID AAF74285 standard; DNA; 2022 BP.
 XX AAF74285;
 AC AAF74285;
 DT 04-MAY-2001 (first entry)
 XX Vigna radiata calcium dependent protein kinase clone.
 DE Vigna radiata calcium dependent protein kinase; CDPK; herbicide resistance;
 KW paraquat; diquat; crop production; ds.
 XX Vigna radiata.
 OS Vigna radiata.
 XX WO200107592-A2.
 PN 01-FEB-2001.
 XX 26-JUL-2000; 2000WO-CB02876.
 XX 27-JUL-1999; 99GB-0017642.
 XX (ZENE) ZENECA LTD.
 XX Holt CD, White AJ, Michael AJ, Osborn RW;
 XX WPI; 2001-168549/17.
 XX Producing herbicide resistance plants by inhibiting calcium dependent
 PT protein kinase in plants or by providing an intracellular vacuolar
 PT transporter capable of transporting agrochemical into plant vacuole
 XX

PS

Claim 18; Page 44-45; 50pp; English.

XX The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance.

XX

SQ Sequence 2022 BP; 587 A; 374 C; 466 G; 595 T; 0 other;

Alignment Scores:

Pred. No.:	1.87e-163	Length:	2022
Score:	1762.00	Matches:	331
Percent Similarity:	82.19%	Conservative:	66
Best Local Similarity:	68.53%	Mismatches:	83
Query Match:	67.95%	Indels:	3
DB:	22	Gaps:	2

US-09-848-806-1 (1-495) x AAF74285 (1-2022)

Qy	5	ProAsnProArgArgPro-SerAsnThrValLeuProTyrGlnThrProArgLeuArgAs	24
Db	102	CGCGGCTTACACACAGGATATATGCTTGGCCATAGACTCCCAACATTGCGTA	161
Qy	24	pHisTyrLeuLeuGlyLysLysLeuGlyGlnGlnPheGlyThrThrTyrLeuCysTh	44
Db	162	TCTATACACTCTTGGCCCAATTTGGGACAGGCAATTTGGCACCACCTTATTATGCAC	221
Qy	44	rGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCy	64
Db	222	CGAAGATTCTACTTCCCAATGATGCTGCAATCTATCTCCAAAAGAAAGTTGATTC	281
Qy	64	sArgGluAspTyrGluAspValTyrArgGluIleGlnIleMethHisLeuSerGluHi	84
Db	282	CAAGGAGATGTCAGGATGTCAGGAGGGAATTCAGATATGATCATTTAGCTGGTCA	341
Qy	84	sProAsnValValArgLysGlyThrTyrGluAspSerValPheValHisIleValMe	104
Db	342	CAAGAACATTTCTACCATTAAGGCTTACAGGATCCTCTCTATGTGCATATAGTCAT	401
Qy	104	tGluValCysGluGlyGlyLeuPheAspArgIleValSerLysGlyHisPheSerGl	124
Db	402	GGAGCTTTGCTGGGGTGGTGTGTGTGATCGCATCATCAGAGGGGCCACTATACCGA	461
Qy	124	uArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLe	144
Db	462	GAGGAAGCTGCAGAGTTGACCAAAATTTGTTGGGGTGTTCAGGCTTGCTATTCCT	521
Qy	144	uGlyValMethHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAs	164
Db	522	TGGGGTCATGCACAGATCTCAAGCCAGAAAACTTTCTTTTGGTCAATAAAGATGATGA	581
Qy	164	pAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLe	184
Db	582	TTTCTCTTAAAGCAATGACTTTGGCCCTCCGGTTTCTTCAAAACCCGGTCAAAATTTT	641
Qy	184	uTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyrGl	204
Db	642	CACATGATGATGCGGACCCATATGTTGCTCCTCCTAGGTTCTCTCAAGCATATGG	701
Qy	204	yProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValPr	224
Db	702	GCCTGAAGCAGACGTGTGGACGCGGTGCATCTGATATTTGCTTAGTGGTGATCC	761
Qy	224	oProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeuAs	244
Db	762	ACCATTTGGCAGAGACCCCAAGATATATTTGATGACAGTATTGAAGGACATATAGA	821
Qy	244	pPheLysSerAspProTrpProThrIleSerGluAlaAlaLysAspLeuIleTyrLysMe	264
Db	822	TTTTTGATCAGATCCTTGGCCCTCTAATATCTGACAGTGGAAAAAGATCTGATCAGAAGAT	881
Qy	264	tLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCysHisProTrpIl	284

Db

882 GCTGTGTTCTCAGCCTTTCAGAACGGTTGACTGCTCATCAAGTGTATGTCTATCTTGGAT

Qy

284 eValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLy

Db

942 ATGTGAAAATGGAGTTGCACCTGACAGGCAATAGACCTGCTGCTCTCTCTCTCTCTAA

Qy

304 sGlnPheSerGlnMetAsnLysLysLysMetAlaLeuArgValIleAlaGluArgLe

Db

1002 ACAGTTTTCTGCAATGAATGAAGTGAAGAAGATGGCATTCGGGTGATGCTGAAGTCT

Qy

324 uSerGluGluGluIleGlyLeuLysGluLeuPheLysMetIleAspThrAspAsnSe

Db

1062 ATCTGAAGAGAGATTTGCTGGATTGAGAGAAATGTTTCAGGCTATGATACCGATAACAG

Qy

344 rGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGlySerGluLeuMe

Db

1122 TGGTGAATCATTCTTTCGAACTCAAAAGCTGGTCTAAGAAGATATGGTCTACCCCTAA

Qy

364 tGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGlyThrIleAs

Db

1182 AGATGTAGAATACGTGATCTGATGGAAGCGGCTGATGTCACAAAAAGTGAACCATAGA

Qy

384 pTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArgGluGluIleLe

Db

1242 TTATGGGAGTATTGCTGCTCAGTTCATCTCAACAACTAGAACGTGAAGAACATCT

Qy

404 uValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThrIleAspGluLe

Db

1302 TATTGACGATCTCAATATTTTGCACAGGATGGCAGTGGTTATATTACGGTTGATGAAT

Qy

424 uGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspMetIleLysGl

Db

1362 TCACAAAGCTTGTGCAGAACATAACACTGACTGATGCTTTCTTGAAGATATTATTAGGA

Qy

444 uIleAspLeuAsnAspGlyLysIleAspPheSerGluPheThrAlaMetMetArgLy

Db

1422 AGTTGATCAAGATAATGATGGAAGGATTTGATTTGTTGTAATTTGCTGCAATGATGCAAA

Qy

464 sGlyAsp---GlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPheAsnIleAl

Db

1482 AGGCAATGCTGGAATGGTAGG---AGGACTAGCGCAATAGTCTGAATTTAAGCATGAG

Qy

483 aAspAla 485

Db

1539 GGACGCA 1545

RESULT 8

AAC42924

ID

AAC42924

AC

AAC42924;

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XX

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PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0128645.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
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PR 01-JUN-1999; 99US-0137222.
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PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
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PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.

PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
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PR 21-JUL-1999; 99US-0145086.
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PR 27-JUL-1999; 99US-0145913.
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PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
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PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 06-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
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PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149930.
PR 23-AUG-1999; 99US-0149902.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151085.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.

XX 21-JAN-2003 (first entry)
 XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2344.
 XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX WO200216655-A2.
 XX 28-FEB-2002.
 XX 24-AUG-2001; 2001WO-US26685.
 XX 24-AUG-2000; 2000US-227866P.
 PR 26-JAN-2001; 2001US-264647P.
 PR 22-JUN-2001; 2001US-30011P.
 XX (SCRI) SCRIPPS RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Harper JF, Kreps J, Wang X, Zhu T;
 XX WPI; 2002-304127/34.
 XX Identifying a stress condition to which a plant cell has been exposed
 PT and producing plants with increased tolerance to these abiotic stresses
 PT
 XX Claim 144; SEQ ID NO 2344; 577pp + Sequence Listing; English.
 XX The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising:
 CC (a) contacting nucleic acid representative of expressed polynucleotides
 CC in the plant cell with an array or probes representative of the plant
 CC cell genome; and
 CC (b) detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 CC specification but is based on sequence information supplied to Derwent by
 CC the European Patent Office.
 XX
 SQ Sequence 1635 BP; 474 A; 283 C; 393 G; 485 T; 0 other;
 Alignment Scores:
 Pred. No.: 1.59e-160 Length: 1635
 Score: 1731.00 Matches: 328
 Percent Similarity: 81.88% Conservative: 65
 Best Local Similarity: 68.33% Mismatches: 85
 Query Match: 66.76% Indels: 2
 DB: 24 Gaps: 2
 US-09-848-806-1 (1-495) x AB214539 (1-1635)
 QY 6 AsnProArgArgProSerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHis 25
 DB 193 AACGTTGACNACAACTTACTACTATGTTCTTGGTCACAAAGACTCCTAACATCGTGATCTT 252
 QY 26 TyrLeuLeuGlyLysLysLeuGlyGlnGlnPheGlyThrThrTyrLeuCysThrGlu 45
 DB 253 TACACGTTGAGTCGTAAGTAGGACAAAGGACAAATTCGGGACACGTAATTGTGTACTGAT 312
 QY 46 LysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArg 65
 DB 313 ATTGCCACACGGGTTTGACTACTGCTTGAAGTCTATATCCAAAGAGGAAATTTGATATCTAAA 372
 QY 66 GluAspTyrGluAspValTrpArgGluIleGlnIleMetHisLeuSerGluHisPro 85
 DB

Db 373 GAAGATGTTGAGGATGTTAGGAGGAGATTTCAGATTATGCATCATTTAGCTGGTCACAAG 432
 QY 86 AsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleValMetGlu 105
 Db 433 AATATTGTTACTATTAAAGGAGCTTATGAGATCCTTTGTATGTTACATTTGATGAGG 492
 QY 106 ValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArg 125
 Db 493 CTTTGTGCTGCTGGTGAGTTGTTGTAGGATTATTCATAGAGGTTCATTACAGCGAGAGG 552
 QY 126 GluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGly 145
 Db 553 AAAGCTGCTGAGTTGACCAAGATCAATTGTCGGTGTGTTGAGCGGTGTCTTCTTCTTGGT 612
 QY 146 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAla 165
 Db 613 GTTATGCATAGAGATTTAAAGCCCTGAGAAATTTCTTGTGTTAATAGGATGATGATTC 672
 QY 166 LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr 185
 Db 673 TCTCTTAAGCCATTGATTTTGTCTCTCTGTTTCTTCAACCCAGGCCAAATATTCAG 732
 QY 186 AspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyrGlyPro 205
 Db 733 GATGTTGTTGAAAGTCCATATGTTGCTCTGAGGTTCCTCTTCTTCTTCTTCTTCTTCTTCT 792
 QY 206 GluLeuAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValPro 225
 Db 793 GAAGCTGATGTGGACTGCTGTTGTTATCTATCTATCTTACTTAAGTGGTGTCCCGCT 852
 QY 226 PheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeuAspPhe 245
 Db 853 TTCTGGCAGAAACACAGCAAGGAATATTTGATGCTGTGTTGAAGGGATATATTGACTTT 912
 QY 246 LysSerAspProTrpProThrIleSerGluAlaLysAspLeuIleTyrLysMetLeu 265
 Db 913 GATACAGACCGTGGCTGTCTATATCCGACAGTCTAAAGATCTGATCCGGAAGATGTA 972
 QY 266 GluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCysHisProTrpIleVal 285
 Db 973 TGCTTAGTCTCTCTGAACTGTTGACGTCTCATGAGTCTTTCGCTCATCGATGATCTGT 1032
 QY 286 AspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGln 305
 Db 1033 GAGAAATGGAGTTGCACCGGATAGAGCACTTGCACCGCTGTTTGTCTCGTCTTAAACAG 1092
 QY 306 PheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAlaGluArgLysSer 325
 Db 1093 TTTTCTGCAATGAATAAATTAAGAGATGGCTTTAAAGGTGATGCTGAGAGCTCTCA 1152
 QY 326 GluGluGluIleGlyLysLeuLysGluPheLysMetIleAspThrAspAsnSerGly 345
 Db 1153 GAAGAGAGATTCGGGTTTAAGAGCNAATGTTGAGGCAATGTTGAGGATCTGATAACAGCGGT 1212
 QY 346 ThrIleThrPheGluLeuLysAlaGlyLeuLysArgValGlySerGluLeuMetGlu 365
 Db 1213 GCAATCAGCTTTGATGAACCTCAAAGCTGGCTTGAGAAAGATATGATCAACCTTGAAGAC 1272
 QY 366 SerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGlyThrIleAspTyr 385
 Db 1273 ACCGAGATCCGAGATCTTATGGAAGCGGCTGATGTGGACAAACAGCGGTACAAATAGATTAC 1332
 QY 386 GlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArgGluGluIleLeuVal 405
 Db 1333 AGCGAGTTTATTCACGCGAGCTCCATCTCGAATAAACTAGAGAGAGAGAGCATCTTGTGC 1392
 QY 406 AlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThrIleAspGluLeuGln 425
 Db 1393 TCTGCAATTCAGTACTTTGACAAAGATGGAAGTGGTTATCATCACCATTGATGAGCTCAA 1452
 QY 426 SerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAspMetIleLysGluIle 445
 Db 1453 CAATCTTGCAATGAGATGGGATGACCGGATGTTTCTTCTTGAAGACATAATCAAAAGATA 1512

Qy 446 AspLeuAspAsnAspGlyValIleAspPheSerGluPheThrAlaMetMetArgIysGly 465
 Db 1513 GATCAAGACACAGTGGACGGATTGATTACGAAGAAATTTGTCGATGATGCAAAAGGGA 1572
 Qy 466 Asp---GlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPheAsnIleAlaAsp 484
 Db 1573 AATGCTGCTGTAGGAGAG--AGAACATGAATAATAGTCTAAACATCAGCATGAGAGAT 1629

RESULT 10

ID ABZ14529 standard; DNA; 1833 BP.

AC ABZ14529;

XX 21-JAN-2003 (first entry)

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2334.

XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX Arabidopsis thaliana.

XX WO200216655-A2.

XX 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US26685.

XX 24-AUG-2000; 2000US-227866P.

XX 26-JAN-2001; 2001US-264647P.

XX 22-JUN-2001; 2001US-300111P.

XX (SCRI) SCRIPPS RES INST.

XX (SYNG) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

XX WPI; 2002-304127/34.

PT Identifying a stress condition to which a plant cell has been exposed

PT and producing plants with increased tolerance to these abiotic stresses

PS Claim 144; SEQ ID NO 2334; 577pp + Sequence Listing; English.

CC The invention relates to identifying a stress condition to which a plant

CC cell has been exposed, comprising:

CC (a) contacting nucleic acid representative of expressed polynucleotides

CC in the plant cell with an array or probes representative of the plant

CC cell genome; and

CC (b) detecting a profile of expressed polynucleotides in the plant cell

CC characteristic of a stress response. The method is useful in the

CC production of transgenic plants, cells and seeds and in producing plants

CC with increased tolerance to abiotic stress. The present sequence is that

CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used

CC in methods of the invention.

CC Note: The sequence data for this patent is not represented in the printed

CC specification but is based on sequence information supplied to Derwent by

CC the European Patent Office.

XX SQ Sequence 1833 BP; 545 A; 346 C; 486 G; 456 T; 0 other;

Alignment Scores:

Pred. No.:	9.04e-160	Length:	1833
Score:	1724.00	Matches:	329
Percent Similarity:	77.89%	Conservative:	62
Best Local Similarity:	65.54%	Mismatches:	91
Query Match:	66.49%	Indels:	20
DB:	24	Gaps:	2

US-09-848-806-1 (1-495) x ABZ14529 (1-1833)

Qy	2	GluThrLysPro-----AsnProArgArgPro-----	10
Db	316	GAGACCAAGCGGAGTCAAAACCTGATCCTCAGCTAAACCTAAGACCTAAACACACATG	375
Qy	11	-----SerAsnThrValLeuProTyGlnThrProArg	21
Db	376	AAGAGAGTGTCAGTGCAGGGCTTAGGACTGAGTCAGTGTTCGAGAGGAGACTCAAAAC	435
Qy	22	LeuArgAspHisTyrLeuLeuGlyLysLeuGlyGlnGlyGlnPheGlyThrThrTyr	41
Db	436	TTCAAGGAATTTCTATTCCTTCGGGAAGGAAATCGGCACAAGGCAATTTGGGACGCACTTTT	495
Qy	42	LeuCyThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLys	61
Db	496	TTATGTGTCGAGAAGACTACCGGGAAGAGATTTCCTCCAAGTCGATTCCTAAGAGGAG	555
Qy	62	LeuValCysArgGluAspTyrGluAspValTyrArgGluIleGlnIleMetHisHisLeu	81
Db	556	CTATTGACTGATGAGGACGTTGAGGATCTGAGAGAGAGAAATTCAGATAATGCATCATTG	615
Qy	82	SerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheValHis	101
Db	616	GCTGGTCACCCCTAATGTCTCATCAAGAGGAGCTTATGAGGATGTTGTGGCAGTGAC	675
Qy	102	IleValMetGluValCysGluGlyGlyLeuPheAspArgIleValSerLysGlyHis	121
Db	676	CTTGTATGAGAGTGTGTGCGAGCGCGAGCTTTTGACAGATCAITCAACCGCGTCAC	735
Qy	122	PheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCys	141
Db	736	TACACAGAGAGAAAGCGGCTGAGCTCACTAGAACCATTTGTTGGGTTGTAGAGCTTGC	795
Qy	142	HisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerPro	161
Db	796	CATTCTCTGTGTGTTATGCATCGAGACCTCAAGCCGAGAAATTTCTGTTGTCTAGTAA	855
Qy	162	LysAspAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGly	181
Db	856	CACGAGATTCCTCTTGAGACGATGATTTTGAGCTCTCCATGTTCTTTAAACACGAC	915
Qy	182	GlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLysLys	201
Db	916	GATGTTTTTACAGATGTTGTTGGTAGCCCATATTATGTTGCCAGAGATTTCTTCGAAG	975
Qy	202	CysTyrGlyProGluIleAspValTyrSerAlaGlyValIleLeuTyrIleLeuLeuSer	221
Db	976	CGTTATGGCCCTGAAAGCTGATGCTGGAGTGTCTGGAGTGTGTGTATATTATTAAGC	1035
Qy	222	GlyValProProPheTyrAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGly	241
Db	1036	GGAGTTCTCCATTTCTGGGCTGAAACCGAACAGGTATTTTCGAACAGGTCTCTCCACGT	1095
Qy	242	LysLeuAspPheLysSerAspProTyrProThrIleSerGluAlaAlaLysAspLeuIle	261
Db	1096	GATCTTGACATTTTCGTCGATCCATGCCAAGTATATCTGAAGTGCACAGGATTTAGTG	1155
Qy	262	TyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuLysHis	281
Db	1156	AGGAAATGCTGTGACGGATCCCAAGAAAGGTTAACTGCCCAAGGATTTATGTGTCAT	1215
Qy	282	ProTyrIleValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeuSer	301
Db	1216	CCATGGGTTCAAGTCGACGGTGTGGCTCCAGACAGGCTTTGGATTCTGCTGTTCTGAGC	1275
Qy	302	ArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAla	321
Db	1276	CGTATGAAGCAGTTTCTGCAATGAACAAGTTCGAAGAAATGGCTCTTAGAGTCATTGCT	1335
Qy	322	GluArgLeuSerGluGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAspThr	341
Db	1336	GAGAGCTTATCTGAAGAAGAAATCGCCGGCTTGAAGAAGAAATGTTTAAATATGATAGATGCG	1395
Qy	342	AspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGlySer	361

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Db 1396 GACACAGTGGTCAGATACTTCGAGAGAACTGAAAGCAGGACTAAACAGTAGGGCGG 1455
QY 362 GluLeuMetGluSerGluLeuLysSerLeuMetAspAlaAlaAspIleAspAsnSerGly 381
Db 1456 AATCTCAAGAGTCTGAAATCTCGACTTTCGACTTTCGACTTTCGACTTTCGACTTTCG 1515
QY 382 ThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArgGlu 401
Db 1516 ACAATAGATTACAAGAGTTTCATAGCTGCAACATTACATCTAAACAAATAAGAGAGAG 1575
QY 402 GluLeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThrIle 421
Db 1576 GACCATTTGTCAGCCCTTTACATACCTTTGACAAAGATGGGCGCGCTATATACCCCA 1635
QY 422 AspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspMet 441
Db 1636 GACGAGCTTCAACAAGCTTTGTGAGGAGTTTGTGTTGAGGATGTCGCCATAGAAGAACTG 1695
QY 442 IleLysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAlaMet 461
Db 1696 ATGCGCGATTTGATCAAGACAAATGACGGCGGAATAGACTACAACAGATTGTGGCGATG 1755
QY 462 MetArgLysGlyAspGlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPheAsn 481
Db 1756 ATGCAGAAAGGAGCATCACAGGAGGACCTGTCAAAATGGGTCTAGAGAAAGCTTTAGC 1815
QY 482 IleAla 483
Db 1816 ATTGCT 1821
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RESULT 11

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AAF74283
ID AAF74283 standard; DNA; 2550 BP.
XX
AC AAF74283;
XX
DT 04-MAY-2001 (first entry)
XX
DE Cucurbita pepo calcium dependent protein kinase clone.
XX
KW Calcium dependent protein kinase; CDPK; herbicide resistance;
KW paraquat; diquat; crop production; ds.
XX
OS Cucurbita pepo.
XX
PN WO200107592-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-GB02876.
XX
PR 27-JUL-1999; 99GB-0017642.
XX
PA (ZENE ) ZENECA LTD.
XX
PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX
XX WPI; 2001-168549/17.
XX
PT Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole
XX
PS Claim 18; Page 43; 50pp; English.
XX
CC The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance.
XX
SQ Sequence 2550 BP; 710 A; 467 C; 627 G; 746 T; 0 other;
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Alignment Scores:
Pred. No.: 3,77e-158 Length: 2550
Score: 1709.50 Matches: 321
Percent Similarity: 80.61% Conservative: 78
Best Local Similarity: 64.85% Mismatches: 17
Query Match: 65.93% Indels: 17
DB: 22 Gaps: 3
US-09-848-806-1 (1-495) x AAF74283 (1-2550)
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QY 4 LysProAsnProArg-----ArgPro----- 10
Db 804 AAACAGAACCCCTATGGAACCGAGGTGCGCCCTTTATGAGAGGGGTGGGTAGTGCT 863
QY 11 -----SerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHisTyrLeu 27
Db 864 GGGCTTCGAGGTGGTTCGGTCTACAGACGAAACCGGAAACTTTAAGGAGTATTATAGC 923
QY 28 LeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThrTyrLeuCysThrGluLysSer 47
Db 924 TTGGGTAAAAAATTAGGCCAAGCAAAATTTGGGACAAATATATGTGTGTGGAGAGGCA 983
QY 48 ThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArgGluAsp 67
Db 984 ACTGGGAAGAGTATGCTTTGTAAGTCTATTGCAAGAGGAAGTTGGTTAATGAGGATGAT 1043
QY 68 TyrGluAspValTyrArgGluIleGlnIleMetHisLysLeuSerGluHisProAsnVal 87
Db 1044 GTTGAAGATGTCAGAGGGAATTTAGATAATGCACCAATTTGTCTGCACACCCGAATGTT 1103
QY 88 ValArgIleLysGlyThrTyrGluAspSerValPheValHisIleValMetGluValCys 107
Db 1104 ATATCGATCAAGCGGGCGGTACGAGGATGCGGTTCAGTTCAGTTCAGTTCAGTTCAGT 1163
QY 108 GluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArgGluAla 127
Db 1164 GCTGGAGGTGAGCTATTTGATAGGATCATTCACAGTGGACATATTACCGAAAGAAAGGCT 1223
QY 128 ValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGlyValMet 147
Db 1224 GCTGAGCTTACTAGGACCATAGTCGGGGTTTTGGAGGCATGTCACGCTCTTGAGTTATG 1283
QY 148 HisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAspAlaLysLeu 167
Db 1284 CACCGTGACCTTAAGCCCGAGAAATTTCTCTTTGTAGCAAGAGAGGAATCACCTTC 1343
QY 168 LysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyrAspVal 187
Db 1344 AAGCAATTGATTTTGGACTATCAATGTTCTTCAACACCGAGCGAAAGTTTAATGATGTG 1403
QY 188 ValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyrGlyProGluIle 207
Db 1404 GTCGGGAGTCCGTACTATGTCACCTGAGTTTTCGGAAGCGATATGGTCCAGAGCA 1463
QY 208 AspValTyrSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValProProPheTyr 227
Db 1464 GATGTTTGGAGTGTGGAGTAATTTGATATACATTTCTTTAAGTGGAGTGCTCCCTTTGG 1523
QY 228 AlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeuAspPheLysSer 247
Db 1524 GCTGAGTCTGAGGAAGGGATATTTGAAGAGGTCTTCACGCGGATCTTGACTCTCTCTCC 1583
QY 248 AspProTyrProThrIleSerGluAlaAlaLysAspLeuIleTyrLysMetLeuGluArg 267
Db 1584 GACCTTGGCCCGAGTCTCCGACAGTCGGAAGATTTGGTTAGAAAGATGCTTGTTCGA 1643
QY 268 SerProLysLysArgIleSerAlaHisGluAlaLeuCysHisProTyrIleValAspGlu 287
Db 1644 GACCCGGAAGAGAGTACACGATATGAAGTTTGTGCCACCCCTTGGTTCAAGTTGAT 1703
QY 288 GlnAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGlnPheSer 307
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Dd	1704	GGTGTGCTCTGACAAAGCCGCTTGACTCGGCAGCTCTTGACTCGCTTTGAAGCAGCTTTTCA	1763	PR	23-APR-1999;	99US-0130891.
Qy	308	GlnMetAsnIysIleTyrLysMetAlaLeuArgValIleAlaGluArgLeuSerGluGlu	327	PR	28-APR-1999;	99US-0131449.
Dd	1764	GCCATGAACAGCTCAAGAAATGCGTATCAAGGTCTTCAGAGAGCTTATCTGAAGAA	1823	PR	30-APR-1999;	99US-0132048.
Qy	328	GluIleGlyGlyLeuLysGluLeuPheLysMetIleAspThrAspAsnSerGlyThrIle	347	PR	04-MAY-1999;	99US-0132484.
Dd	1824	GAATTCGTGACTCAAGAAATGTTCAAGATGATAGTACTGACACAGCGGCAATC	1883	PR	05-MAY-1999;	99US-0132485.
Qy	348	ThrPheGluGluLeuLysAlaGlyLeuLysArgValGlySerGluLeuMetGluSerGlu	367	PR	06-MAY-1999;	99US-0132486.
Dd	1884	ACATTTCAAGAACTCAAGCTGGATTGAAAAAGTTTGGAGCTAATCTTAAGGAGTCGCA	1943	PR	06-MAY-1999;	99US-0132487.
Qy	368	IleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGlyThrIleAspTyrGlyGlu	387	PR	07-MAY-1999;	99US-0132863.
Dd	1944	ATTTACCACTAATGCAAGCAGCGGATATAGAACACCGAACCATCGACTACGGGGAG	2003	PR	11-MAY-1999;	99US-0134256.
Qy	388	PheLeuAlaIleThrLeuHisMetAsnMetGluArgGluGluIleLeuValAlaAla	407	PR	14-MAY-1999;	99US-0134218.
Dd	2004	TTCTAGCTGCCACATTGCACTCTAAACAAATCGAAGGAAGATCATCTTCTAGCAGCG	2063	PR	14-MAY-1999;	99US-0134221.
Qy	408	PheSerAspPheAspLysAspGlySerGlyTyrIleThrIleAspGluLeuGlnSerAla	427	PR	18-MAY-1999;	99US-0134370.
Dd	2064	TTTTCATATTTCGACAAAGATGGAAGCGGTTCAATACCGACGAGCTTCAACAAGCA	2123	PR	18-MAY-1999;	99US-0134376.
Qy	428	CysThrGluPheGlyLeuCysAspThrProLeuAspAspMetIleLysGluIleAspLeu	447	PR	19-MAY-1999;	99US-0134941.
Dd	2124	TGTAAGAGTTCCGATAGAGGATCTCAATGGAAGAATGATGCCGAGGTCGATCAA	2183	PR	21-MAY-1999;	99US-0135124.
Qy	448	AspAsnAspGlyLysIleAspPheSerGluPheThrAlaMetMetArgLysGlyAspGly	467	PR	24-MAY-1999;	99US-0135353.
Dd	2184	AACAATGACGGAAGCATCGACTACTAAGAGTTCTGTGGCGATGATGCAAAAAGGAATGTA	2243	PR	25-MAY-1999;	99US-0136021.
Qy	468	ValGlyArgSerArgThrMetMetLysAsnLeuAsnPheAsnIle	482	PR	27-MAY-1999;	99US-0136392.
Dd	2244	GTGAATCTGCGAAGAAAGCGCTACAAAGT---AGCTTCAGCAAT	2285	PR	28-MAY-1999;	99US-0136782.
RESULT 12				PR	01-JUN-1999;	99US-0137222.
AAC45753				PR	04-JUN-1999;	99US-0137528.
ID AAC45753 standard; DNA; 3054 BP.				PR	07-JUN-1999;	99US-0137724.
XX AAC45753;				PR	08-JUN-1999;	99US-0138094.
XX				PR	10-JUN-1999;	99US-0138540.
DT 18-OCT-2000 (first entry)				PR	14-JUN-1999;	99US-0139119.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 47639.				PR	16-JUN-1999;	99US-0139452.
XX				PR	16-JUN-1999;	99US-0139453.
KW Hybridisation assay; genetic mapping; gene expression control;				PR	17-JUN-1999;	99US-0139492.
KW protein identification; signal transduction pathway;				PR	18-JUN-1999;	99US-0139454.
KW metabolic pathway; promoter; termination sequence; ss.				PR	18-JUN-1999;	99US-0139455.
XX Arabidopsis thaliana.				PR	18-JUN-1999;	99US-0139456.
XX				PR	18-JUN-1999;	99US-0139457.
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XX				PR	18-JUN-1999;	99US-0139461.
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XX				PR	18-JUN-1999;	99US-0139463.
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XX				PR	23-JUN-1999;	99US-0140353.
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XX				PR	29-JUN-1999;	99US-0140991.
XX				PR	30-JUN-1999;	99US-0141287.
XX				PR	01-JUL-1999;	99US-0141842.
XX				PR	02-JUL-1999;	99US-0142154.
XX				PR	06-JUL-1999;	99US-0142390.
XX				PR	08-JUL-1999;	99US-0142803.
XX				PR	09-JUL-1999;	99US-0142920.
XX				PR	12-JUL-1999;	99US-0142977.
XX				PR	13-JUL-1999;	99US-0143542.
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XX				PR	19-JUL-1999;	99US-0144331.
XX				PR	19-JUL-1999;	99US-0144332.
XX				PR	19-JUL-1999;	99US-0144333.
XX				PR	19-JUL-1999;	99US-0144334.
XX				PR	19-JUL-1999;	99US-0144335.
XX				PR	20-JUL-1999;	99US-0144352.
XX				PR	20-JUL-1999;	99US-0144632.

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PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
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PR 23-JUL-1999; 99US-0145145.
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PR 23-JUL-1999; 99US-0145224.
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PR 27-JUL-1999; 99US-0145913.
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PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
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PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
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PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
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PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
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PR 04-OCT-1999; 99US-0157117.
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PR 06-OCT-1999; 99US-0157865.
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PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
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PR 14-OCT-1999; 99US-0159329.
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PR 14-OCT-1999; 99US-0159637.

PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:
Pred. No.: 2,1e-157
Score: 1703.00
Percent Similarity: 78.66%
Best Local Similarity: 65.65%
Query Match: 65.68%
DB: 21

US-09-848-806-1 (1-495) x AAC45753 (1-3054)

Qy 2 GluThrLysProAsnProArgArgPro----- 10
Db 1525 GAGACGAAAGCTGACCTCAGAGCCCTAACATATGAGGAGGTGTCAGTGCAGGCGTT 1584
Qy 11 ---SerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHisTyrLeuGly 29
Db 1585 AGAACTGAGTCAGTGTTCAGAGGAAACTGAAAACTTTAAGGAGTCTTATTATTAGG 1644
Qy 30 LysIleLeuGlyGlnGlyGlnPheGlyThrTyrLeuCysThrGluLysSerThrSer 49
Db 1645 AGGAACTTGGCAAGGGCAATTTGGGACACGCTTTTATGCCCTTGAGAAAGTACTGGG 1704
Qy 50 AlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArgGluAspTyrGlu 69
Db 1705 AACGAATATCGTGCAAGTCGATTTCCAGAGAGGAGCTTTTGACTGATGAGGATGTGAA 1764
Qy 70 AspValTrpArgGluIleGlnIleMetHisLeuSerGluHisProAsnValValArg 89
Db 1765 GATGTGAGAAGAGAGATTCAGATAATGTCATCCTGGCTGGTCATCCGAATGTTATATCT 1824
Qy 90 IleLysGlyThrTyrGluAspSerValPheValHisIleValMetGluValCysGluGly 109
Db 1825 ATTAAGGTGCTTATGAGGATGTTGTGCGGTACATCTTGTGATGGAGTGTGTGTCGGT 1884
Qy 110 GlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArgGluAlaValLys 129
Db 1885 GCGGAGCTTTTGATAGAAATTATTCAACGTGGACATTACACTGAGAGAAAGCTGCTGAG 1944
Qy 130 LeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGlyValMetHisArg 149
Db 1945 CTTGCGAGAACCACTTGTGGGTTTATAGAGCTTGTCACTCTCTTGGTGTATGATCGG 2004
Qy 150 AspLeuLysProGluAsnPheLeuPheAspSerProLysAspAlaLysLeuLysAla 169
Db 2005 GACCTCAAGCAGAGAAATTTCTATTGTTAGTAGAGAGAGAGATTCCTCTGTTGAAACG 2064
Qy 170 ThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyrAspValValGly 189
Db 2065 ATCGACTTTGGACTCTCAATGTTCTTTAAGCCAGATGAGGTTTTTACAGATGTTGTGGT 2124
Qy 190 SerProTyrTyrValAlaProGluValLeuLysCysTyrGlyProGluIleAspVal 209
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Db 2125 AGTCGATATTATGTAGCTCCAGAACTTCTTAGAAGCGTTATGGTCCTGAATCATCATGTG 2184
Qy 210 TrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValProProPheTrpAla--- 228
Db 2185 TGGAGTGTGTGTGTGATTTTACATTTTGTAAAGCGAGTTCTCTCTTCTGGCCGCGC 2244
Qy 229 -----GluThrGluSerGlyIlePheArgGln 237
Db 2245 TCTGAGTAATAATTTGTTTCCATGAATAATATACAGAAACCGAAGGATTTTTCAGGAG 2304
Qy 238 IleLeuGlnGlyLysLeuAspPheLysSerAspProTrpProThrIleSerGluAlaAla 257
Db 2305 GTCCTTTCAGAGATCTTTCATCTGATCCATGCGCAAGCATCTCTGAAAGCGG 2364
Qy 258 LysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGlu 277
Db 2365 AAAGACTTGGTAAGGAAATGCTTGTTCGAGACCCCAAGCGAAGACTAACCCGCACATCAA 2424
Qy 278 AlaLeuCysHisProTyrIleValIleAspGluGlnAlaAlaProAspLysProLeuAspPro 297
Db 2425 GTATTATGTCATCCATGGGTACAGATTGACGGTGTGGCTCCAGATAAACCTCTGGACTCT 2484
Qy 298 AlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeu 317
Db 2485 GCTGTCTCTGAGCGGTATGAAGCAATTTCTGCAATGAACAAGTTCAAGAAAATGGCTCTT 2544
Qy 318 ArgValIleAlaGluArgLeuSerGluGluIleGlyLeuLysGluLeuPheLys 337
Db 2545 AGAGTCATAGCTGAGAGTTTCTGAGAGAAATAGCGGGTTTAAACAAATGTTCAAG 2604
Qy 338 MetIleAspThrAspAsnSerGlyThrIlePheGluGluLeuLysAlaGlyLeuLys 357
Db 2605 ATGATAGACGACAGACAATAGTGGTCAGATCACTTTTGAAGAACTGAAGACGAGGACTAAA 2664
Qy 358 ArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIle 377
Db 2665 CGAGTGTGTGCAATCTCAAGAGAGTCAGAGATTCTTGATCTAATGCAAGCTGCTGATGTG 2724
Qy 378 AspAsnSerGlyThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLys 397
Db 2725 GACAAATAGCGAAGCATAGACTACAAAGATTTCATAGCCGCCAATTCATCTCAACAAA 2784
Qy 398 MetGluArgGluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGly 417
Db 2785 ATAGAGAGAGAGGACCAATTTGTCGCCCTTCTCTTACTTTGACAGGACGAGAGTGGC 2844
Qy 418 TyrIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrPro 437
Db 2845 TTTATCACCCCGGACGAGCTTCAACAAGCTTTCGAAAGAGTTTGGTGTGAAGATGCCCGC 2904
Qy 438 LeuAspAspMetIleLysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGlu 457
Db 2905 ATAGAAGAAATGATCGCGATGTTGATCAAGCAAGGATGGAAGTGAAGTACATCAACGAG 2964
Qy 458 PheThrAlaMetMetArgLysGlyAspGlyValGly 469
Db 2965 TTTTGCAATGATGCAAGAAAGGAGCATATGCGA 3000
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RESULT 13

AAF74277

ID AAF74277 standard; DNA; 2334 BP.

AC AAF74277;

XX 04-MAY-2001 (first entry)

DT Rice calcium dependent protein kinase clone #1.

DE Calcium dependent protein kinase; CDPK; herbicide resistance;

XX paraquat; diquat; crop production; ds.

KW Oryza sativa.

XX

OS

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XX WO200107592-A2.
PN 01-FEB-2001.
XX 26-JUL-2000; 2000WO-GB02876.
XX 27-JUL-1999; 99GB-0017642.
XX (ZENE ) ZENECA LTD.
XX Holt CD, White AJ, Michael AJ, Osborn RW;
XX WPI; 2001-168549/17.
XX Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole
XX Claim 18; Page 39; 50pp; English.
XX The present invention describes a method of producing plants which are
CC resistant to the herbicides paraquat and diquat, involving inhibiting in
CC the plants a calcium dependent protein kinase (CDPK) and selecting those
CC plants which are resistant to the agrochemical of interest. This is
CC useful in the production of crops with herbicide resistance.
XX Sequence 2334 BP; 659 A; 430 C; 625 G; 620 T; 0 other;
SQ Alignment Scores:
Pred. No.: 4.83e-146 Length: 2334
Score: 1586.00 Matches: 304
Percent Similarity: 78.35% Conservative: 68
Best Local Similarity: 63.87% Mismatches: 102
Query Match: 61.16% Indels: 2
DB: 22 Gaps: 2
US-09-848-806-1 (1-495) x AAF74277 (1-2334)
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Qy 11 SerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHisTyrLeuLeuGlyLys 30
Db 537 TCTATCAATGTCTTGGCGGAGACAGACGCGACCTAAGGGAGCATATATCATCTGTCGG 596
Qy 31 LysLeuGlyGlnGlyGlnPheGlyThrThrTyrLeuCysThrGluLysSerThrSerAla 50
Db 597 AAGCTTGTGAGGCCCTAGTTTGGCACAACATTTACCTCTGTACCGAGATCAATACAGGGTGT 656
Qy 51 AsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArgGluAspTyrGluAsp 70
Db 657 GAGTATGCTTGCAGACCATCCCAAGCGCAAGCTCATCAACAGGAGGATGTAGAGAT 716
Qy 71 ValTrpArgGluIleGlnIleMetHisLeuSerGluHisProAsnValValArgIle 90
Db 717 GTGCGCGTGAGATTTCAGATAATGCACCAATTTGTGCGGCCCAACAAGAAATGTTGTTGCAATC 776
Qy 91 LysGlyThrTyrGluAspSerValPheValHisIleValMetGluValCysGluGly 110
Db 777 AAGGATGCTATGAGGATGGCAAGCGGTGCACATTTGTATGGAGCTCTGCGCTGTCGG 836
Qy 111 GluLeuPheAspArgIleValSerLysGlyHisPheSerGluArgGluAlaValLysLeu 130
Db 837 GAGCTCTTTCAGAGATTTCAGGAGAGGGGCATTTACAGCGAGCGGAGGCTGCAGAGCTT 896
Qy 131 IleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGlyValMetHisArgAsp 150
Db 897 ATAAGATAAATTTGTCAGCATTTGTGCTATGTCCTTCGCTCGGGGTGATGCACCGTAT 956
Qy 151 LeuLysProGluAsnPheLeuPheAspSerProLysAspAlaLysLeuLysAlaThr 170
Db 957 CTTAAGCCAGAAAATTTCTCTCTTTTGGATAAAGATGATGATCTGTCATAAAGGCAATA 1016
Qy 171 AspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyrAspValValGlySer 190
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Db 1017 GATTTTGGCTATCCGTTGTTCTTCAAAACAGGTCAGGTTTTTCACTGAGCTGGTTGGAGT 1076
QY 191 ProTyrTyrValAlaProGluValLeuLeuLysCysTyrGlyProGluIleAspValTyr 210
Db 1077 CCATATTATGTTCTCTAGGTTATGCAACAAGCTTATGACAGAACTCTGATGTGTGG 1136
QY 211 SerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValProPheTyrAlaGluThr 230
Db 1137 TCAGCTGGAGTATACCTTTACGTTTGTCTGAGTGGAGTGCACCATTTTGGGAGAGACA 1196
QY 231 GluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeuAspPheLysSerAspProTyr 250
Db 1197 CAACAAGGATATTTGATGAGTCTCTGAAGGTCACATTTTCAATCTGATCCATGG 1256
QY 251 ProThrIleSerGluAlaLysAspLeuIleTyrLysMetLeuGluArgSerProLys 270
Db 1257 CCAAGATATCTGACAGTGCAGAGGATCTTATAAGAAAAATGCTCTCTCATTTGCCCTTCG 1316
QY 271 LysArgIleSerAlaHisGluAlaLeuCysHisProTyrIleValAspGluGlnAlaAla 290
Db 1317 GAGCGTTTGAAGCCCATGAAGTGTCTAAGGCATCTTGGATCTGTGAAATATGGAGTTGCC 1376
QY 291 ProAspLysProLeuAspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsn 310
Db 1377 ACTGATCAAGCTCTGGATCCAGTGTATCTCTCGGCTCAAAATCTCTGCAATGAAC 1436
QY 311 LysIleLysLysMetAlaLeuArgValIleAlaGluArgLeuSerGluGluIleGly 330
Db 1437 AAGTTAAAGAAAGTGGCTCTGAGAGTGATAGCTGAGCGTCTTTTCAGAGGAGGAGATTGCT 1496
QY 331 GlyLeuLysGluLeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGlu 350
Db 1497 GGGTTAAGAGAAATGTTTCAAGCGCAGTGGACACAAAAATAGAGGTGTATTCACCTTTCGGT 1556
QY 351 GluLeuLysAlaGlyLeuLysArgValGlySerGluLeuMetGluSerGluIleLysSer 370
Db 1557 GAGCTTAGAGAAAGTTTAAAGATTTTGGCGTGAATTTAAGGATACAGAGATTGGTAT 1616
QY 371 LeuMetAspAlaAlaAspIleAspAsnSerGlyThrIleAspTyrGlyGluPheLeuAla 390
Db 1617 ATAATGGAAGCGGCACACACGACAAATATGTAAACATCCATTTATGAAGAAATTTATTGCT 1676
QY 391 AlaThrLeuHisMetAsnLysMetGluArgGluGluIleLeuValAlaAlaPheSerAsp 410
Db 1677 GCNACTCTACCTTTAACAGATAGAACGTGAGAGCACCTCTGTCGAGCTTTTACATAT 1736
QY 411 PheAspLysAspGlySerGlyTyrIleThrIleAspGluLeuGlnSerAlaCysThrGlu 430
Db 1737 TTTGACAAAGATGGGAGTGGTTATATACAGTTGACAGCTTCAACAGCTTGTGGAGAA 1796
QY 431 PheGlyLeuCysAspThrProLeuAspAspMetIleLysGluIleAspLeuAspAsnAsp 450
Db 1797 CATAACATGGAGGATTCACCTCTTGAAGAGATTATTTTCAGAGGTTCATCAAAACAATGAC 1856
QY 451 GlyLysIleAspSerGluPheThrAlaMetMetArgLysGlyAspGlyValGlyArg 470
Db 1857 GGCCAAATTTGACTACCCCAATTTTGGCCATGATG---CAAGGCGACCACTGGACTA 1913
QY 471 Ser---ArgThrMetMetLysAsnLeuAsnPheAsnIleAlaAspAla 485
Db 1914 GGGTGGCAACAATGGAAGCAGTTTGAATGTAGCATTAAAGACGCCA 1961
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RESULT 14

AAF74281

ID AAF74281 standard; DNA; 1647 BP.

XX

AC AAF74281;

XX

DT 04-MAY-2001 (first entry)

XX

DE Liverwort calcium dependent protein kinase clone #1.

XX

KW Calcium dependent protein kinase; CDPK; herbicide resistance;

XX paraquat; diquat; crop production; ds.

XX Marchantia polymorpha.

XX WO200107592-A2.

XX 01-FEB-2001.

XX 26-JUL-2000; 2000WO-GB02876.

XX 27-JUL-1999; 99GB-0017642.

XX (ZENE) ZENECA LTD.

XX Holt CD, White AJ, Michael AJ, Osborn RW;

XX WPI; 2001-168549/17.

XX Producing herbicide resistance plants by inhibiting calcium dependent protein kinase in plants or by providing an intracellular vacuolar transporter capable of transporting agrochemical into plant vacuole

XX Claim 18; Page 42; 50pp; English.

XX The present invention describes a method of producing plants which are resistant to the herbicides paraquat and diquat, involving inhibiting in the plants a calcium dependent protein kinase (CDPK) and selecting those plants which are resistant to the agrochemical of interest. This is useful in the production of crops with herbicide resistance.

XX Sequence 1647 BP; 447 A; 349 C; 465 G; 386 T; 0 other;

Alignment Scores:

Pred. No.: 7 01e-141 Length: 1647

Score: 1531.50 Matches: 294

Percent Similarity: 76.72% Conservative: 75

Best Local Similarity: 61.12% Mismatches: 105

Query Match: 59.06% Indels: 7

DB: 22 Gaps: 3

US-09-848-806-1 (1-495) x AAF74281 (1-1647)

QY 1 MetGluThrLysProAsnProArgArgProSerAsnThrValLeuProTyrGlnThrPro 20

Db 169 ATCTCTGCCAAACAAAGGCCACGTTGACTGGCAAT---GTGCTCGCAGCCACTGGAA 225

QY 21 ArgLeuArgAspHisTyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThr 40

Db 226 GATGTCGATGCCATTTTACACCTCGGACGGGAACCTGGTGTGTTGTTGTCACG 285

QY 41 TyrLeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArg 60

Db 286 CATTTGTGTACGCACCAAGGTTACAGGTGAGCTTTTAGCTTGAAGTCAATTCGCAAGAGG 345

QY 61 LysLeuValCysArgGluAspTyrGluAspValTyrArgGluIleGlnIleMetHisHis 80

Db 346 AAGTTGACCAATAAGGATGACGTAGAGGATGTTTCGGAGGGGAAGTCAGATCATGCACCAC 405

QY 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100

Db 406 TTAGAGGGGCAGAGAACATTTGCGAATTTGAAGGGGGCCCTATGAGGATAAACCAACGTG 465

QY 101 HisIleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGly 120

Db 466 CATCTCGTCATGAGCTTTGCTGCGGAGAACTCTTCGACCGCAATATTACGCGGGGC 525

QY 121 HisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAla 140

Db 526 CACTACAGTGAGAGGGCTGCTGCAGCTCTATGTAGAACTATAGTCAAGTGGTTTCAGACG 585

QY 141 CysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSer 160

Db 586 TGCCATTCTCTGGGAGTTATGCACCGGGATCTGAAAGCCCGAGAAATTTCTGCTTGTCTAAC 645

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QY 161 ProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysPro 180
DB 646 AAGAGGAGGAGTGCACCCCTGAAGGCGAGCATTTTGGTCTTCTCTTCAAGCCT 705
QY 181 GlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLys 200
DB 706 GGAGAGGTTTACAGATATCGTTGGAAGTCTTACTACGTGGCACAGAGGTTTGGT 765
QY 201 LysCysTyrGlyProGluLysLeuLysValTrpSerAlaGlyValLeuLysLeuLys 220
DB 766 CGTAACATATGGCCGAGAGGCTGATGTTGGAGTCCCGGAGTCATTTCTTACATCTTTT 825
QY 221 SerGlyValProProPheThrAlaGluThrGluSerGlyPhePheArgGlnIleLeuGln 240
DB 826 TCGGAGTCCCTCTCTTCTGGCAGAACCCGACACGAGTATTTTGTGCGCTAATGCAC 885
QY 241 GlyLysLeuAspPheLysSerAspProTrpProThrIleSerGluAlaLysAspLeu 260
DB 886 GGTCAATATTGATTTCACTAGTATCTTGGCTTCAATTTCTCAAAAGCGCAAGATCTG 945
QY 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLysCys 280
DB 946 GTAAAGAGGATGCTCAACAGAACCCAAAGAGGCGATTGACGGCCCATGAAATTTAAGT 1005
QY 281 HisProTrpIleValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeu 300
DB 1006 CACCATGATTTAGTGTGCGGAGAGCCACAGACCAACACCTTGACACCGCGTGTG 1065
QY 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysMetAlaLeuArgValIle 320
DB 1066 TCTAGATTGAAGCAATTCACCGCTATGAACAAAGCTCAAGAACTTGTCTCAAGTTATC 1125
QY 321 AlaGluArgLeuSerGluGluLysGlyLeuLysGluLeuPheLysMetIleAsp 340
DB 1126 GCAGAGAGTCTCTCTGAAGAAGAGATCATGGGATTGAAGGAGATGTTTAAAGATGAGC 1185
QY 341 ThrAspAsnSerGlyThrIleThrPheGluLeuLysAlaGlyLeuLysArgValGly 360
DB 1186 ACAGACAACAGTGTGTACAACTCACGTCGAGGAGTTGAAGGATGTTCTCAAAAGCAGGA 1245
QY 361 SerGluLeuMetGluSerGluLysSerLeuMetAspAlaAlaAspIleAspAsnSer 380
DB 1246 TCAAACTGCGAGAGTCAGAGTCCGCGAGCTAATGGCAGCTGCTGATGGATGGAAT 1305
QY 381 GlyThrIleAspTyrGlyGluPheLeuAlaThrLeuHisMetAsnLysMetGluArg 400
DB 1306 GGCACTATTGACTACTTGGAGTTTCATACGGCAACCATGCATTTGAATAAGATAGAAG 1365
QY 401 GluGluLeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThr 420
DB 1366 GAAGATCATCTTTACGCTGCTTTTCAGCATTTTTCAGGACAGCAGCTGGGTTTCATCACC 1425
QY 421 IleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAsp---ThrProLeuAsp 439
DB 1426 ATGAAGAGCTTGAACAGGCTTTAATTAAGCAGCGGATGGAGATCTGTACTCTGAAA 1485
QY 440 AspMetIleLysGluIleAspLeuAspAspGlyLysIleAspPheSerGluPheThr 459
DB 1486 GAAATTTATAGGAGGTTGACATGATCATGATGACGATCACTACACGAGGTTGCTT 1545
QY 460 AlaMetMetArgLysGly-----AspGlyValGlyArgSerArgThrMet 474
DB 1546 GCCATGATGCGTAAAGGTACCCCTGGACACCAAGAGGCGCACAGGAGGATATAAGTAAT 1605
QY 475 Met 475
DB 1606 ATG 1608
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RESULT 15
AAF74282
ID AAF74282 standard; DNA; 1647 BP.
XX

```
AC AAF74282;  
DT 04-MAY-2001 (first entry)  
DE Liverwort calcium dependent protein kinase clone #2.  
KW Calcium dependent protein kinase; CDPK; herbicide resistance;  
KW paraquat; diquat; crop production; ds.  
OS Marchantia polymorpha.  
PN WO200107592-A2.  
XX  
PD 01-FEB-2001.  
XX  
PP 26-JUL-2000; 2000WO-GB02876.  
XX  
PR 27-JUL-1999; 99GB-0017642.  
XX  
PA (ZENE ) ZENECA LTD.  
XX  
PI Holt CD, White AJ, Michael AJ, Osborn RW;  
XX WPI; 2001-168549/17.  
XX  
PT Producing herbicide resistance plants by inhibiting calcium dependent  
PT protein kinase in plants or by providing an intracellular vacuolar  
PT transporter capable of transporting agrochemical into plant vacuole -  
PS Claim 18; Page 42; 50pp; English.  
XX  
CC The present invention describes a method of producing plants which are  
CC resistant to the herbicides paraquat and diquat, involving inhibiting in  
CC the plants a calcium dependent protein kinase (CDPK) and selecting those  
CC plants which are resistant to the agrochemical of interest. This is  
CC useful in the production of crops with herbicide resistance.  
XX  
SQ Sequence 1647 BP; 445 A; 348 C; 464 G; 390 T; 0 other;
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Best Local Similarity: 60.91% Mismatches: 107  
Query Match: 58.79% Indels: 7  
DB: 22 Gaps: 3  
US-09-848-806-1 (1-495) x AAF74282 (1-1647)
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DB 169 ATCTCTGCCAACAAGAGCCACGTTGACTGGCAAT---GTGCTCGCAGGCCACTGGAA 225  
QY 21 ArgLeuArgAspHisTyrLeuLeuGlyLysLeuGlyGlnGlyGlnPheGlyThrThr 40  
DB 226 GATGTGCGATCCATTATACACCTCGGACGGAACTGGGTCTGTCAGTTTGGTGTACG 285  
QY 41 TyrLeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArg 60  
DB 286 CATTTGTGTACGCACCAAGGTTACAGGTGAGCTTTTAGCCCTGCAAGTCAATTCGAAGAGG 345  
QY 61 LysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMetHisHis 80  
DB 346 AAGTTTACCCTAAGGATGACGTAGAGGATGTTTCGGAGGGAAGTGCAGATCATGCACCC 405  
QY 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100  
DB 406 TTAGAGGGGCGAGAGAACATTTGTCGAATTCGAGGGGCGCTATGAGGATAACACACAGCTG 465  
QY 101 HisIleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGly 120  
DB 466 CATCTGCTATGGAGCTTTTGTGTGCGGAGAACTCTTCGACCGGCACTATTTCAGCGGGC 525
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Qy 121 HisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAla 140
Db |||
1606 ATG 1608
Qy 526 CACTACAGTCGAGGGCTCTCGAGCTCTATGTAGAACTATATAGTCGAAGTGGTTTCAGAGC 585
Db |||
Qy 141 CysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSer 160
Db |||
586 TGCCATTCTCTGGGATTATGACCGGATCTGAAGCCCGAGAAATTTCTGCTTCTCAAGCCT 645
Qy 161 ProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysPro 180
Db |||
646 AAGAAGGAGGATGCACCCCTGAAGCGCAGGATTTTGGTCTTCTCTTCAAGCCT 705
Qy 181 GlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLys 200
Db |||
706 GGAGAAGTGTTTACAGATATCGTTGGAAGTGCTTACTAGTGGCACACGAGGTTTTCGCT 765
Qy 201 LysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu 220
Db |||
766 CGTAACATATGGCCAGAGCTGATGTTGGAGTGCCGGAGTCATCTTTACATCTTTTTC 825
Qy 221 SerGlyValProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGln 240
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Qy 241 GlyLysLeuAspPheLysSerAspProTrpProThrIleSerGluAlaLysAspLeu 260
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Qy 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCys 280
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Qy 281 HisProTrpIleValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeu 300
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1006 CACCCATGATATTAGTGTTCACGAGAGGAGCACCAGACAAACCACTTGACACGCCGTG 1065
Qy 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIle 320
Db |||
1066 TCTAGATTGAGCAATTCACCCCTATGAACAAGCTCAAGAACTTGCTCTGAAGGTATC 1125
Qy 321 AlaGluArgLeuSerGluGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAsp 340
Db |||
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Db |||
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Qy 361 SerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSer 380
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Qy 381 GlyThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArg 400
Db |||
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Qy 401 GluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThr 420
Db |||
1366 GAGGATCATCTGTATGCTGCCTTCCAACACTTTGATGGGGAACAACAGTGGGTTTCATCACC 1425
Qy 421 IleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAsp--ThrProLeuAsp 439
Db |||
1426 ATGGAGAGCTTGAACAGGCTTTAATTAAACAGCGGATGGGAGATCCTGATACTCTGAAA 1485
Qy 440 AspMetIleLysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThr 459
Db |||
1486 GAAATATTAGGAGGTTGACACTCATGATGACGCAATCAACTACGACGAGTTCGTT 1545
Qy 460 AlaMetMetArgLysGly-----AspGlyValGlyArgSerArgThrMet 474
Db |||
1546 GCCATGATGCGTAAGGTACCCCTGGACACCAAGAGGGCCACAGGAGGATATAAGTAAT 1605
Qy 475 Met 475
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Db |||
1606 ATG 1608

Search completed: November 28, 2003, 10:56:57
Job time : 473 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 28, 2003, 10:43:12 ; Search time 3093 Seconds
(without alignments)
3889.659 Million cell updates/sec

Title: US-09-848-806-1
Perfect score: 2593
Sequence: 1 METKNPRPSNTVLPYQTP.....KNLNFNIADAFGVDSKSDS 495

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO.spool/US09848806/runat_28112003_103143_2347/app_query.fasta_1.647
-DB=EST -OFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0 -LOOPECL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=plc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09848806 @CNC_1_1_2810 @runat_28112003_103143_2347 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
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19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
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25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1560	60.2	2380	11	AY109473	AY109473 Zea mays
2	1557	60.0	2566	11	AY109374	AY109374 Zea mays
3	1460	50.3	2298	11	AY109401	AY109401 Zea mays
C	4	1362.5	52.5	1628	11	AY109463 Zea mays
	5	1125	43.4	835	10	BG647837 EST509456
	6	1123	43.3	814	12	BG878737 EST513724
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	8	1059.5	40.9	742	10	BG596613 EST495291
	9	1011	39.0	697	12	BJ302783 BJ302783
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	11	984.5	38.0	813	12	BM779035 EST589610
	12	979	37.8	686	12	B1178776 EST519721
	13	961	37.1	751	13	BQ865474 QCSA16.Y
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	16	956	36.9	844	14	CB671831 OSJNFe05J
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	18	951	36.7	800	14	CB659052 OSJNFe15K
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	22	924	35.6	864	14	CB894498 EST647290
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	24	920	35.5	748	13	BQ967112 QHB28P17
	25	907	35.0	750	13	BQ916638 QHB18118
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	39	881	34.0	713	13	BQ801121 WHE2810_E
	40	876	33.8	745	14	CB674516 OSJNFe03J
	41	874.5	33.7	695	10	BE660679 7-C2 Gmax
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ALIGNMENTS

RESULT 1

AY109473

LOCUS

DEFINITION

AY109473

ACCESSION

AY109473.1

VERSION

KEYWORDS

SOURCE

ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 2380)

AY109473 Zea mays 2380 bp mRNA linear HTC 17-OCT-2002

AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 2380)
AUTHORS Coe, E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="MaizeDB:630671"
 /db_xref="taxon:4577"
 /clone_lib="Maize Mapping Project/DuPont Consensus Library"
 /notes="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
 BASE COUNT 478 a 560 c 507 g 468 t 367 others
 ORIGIN

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 Score: 1560.00 Matches: 303
 Percent Similarity: 76.30% Conservative: 48
 Best Local Similarity: 65.87% Mismatches: 107
 Query Match: 60.16% Indels: 2
 DB: 11 Gaps: 2

US-09-848-806-1 (1-495) x AY109473 (1-2380)

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 QY 46 LysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArg 65
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 QY 66 GluAspTyrGluAspValTrpArgGluGlnIleMetHisHisLeuSerGluHisPro 85
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 Db 807 AACGTGCTCGCCATCAAGGGCGCTACGAGGACCATCTCTCGTCCACATCGNNNNNNN 866
 QY 106 ValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArg 125
 Db 867 NNN 926
 QY 126 GluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGly 145
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 QY 186 AspValValGlySerProTyrTyrValAlaProGluValLeuLysCysTyrGlyPro 205
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 QY 346 ThrIleThrPheGluLeuLysAlaGlyLeuLysArgValGlySerGluLeuMetGlu 365
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 QY 426 SerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAspMetIleLysGluIle 445
 Db 1827 CAAGCTTGCAAGAGCATAACTGCGGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1886
 QY 446 AspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAlaMetMetArgLysGly 465
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 QY 466 Asp---GlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPheAsnIleAlaAsp 484
 Db 1947 AATATGGAGTCCGTCGA---AGAAACAATGAGAAACAGCTTGAATATCAGCATGAGGAC 2003

RESULT 2

AY109374
 LOCUS CL146_1 mRNA 2566 bp linear HTC 17-OCT-2002
 DEFINITION Zea mays
 ACCESSION AY109374
 VERSION AY109374.1 GI:21213078
 KEYWORDS HTC.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 2566)

Haun, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.

Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes

Unpublished (2002)

2 (bases 1 to 2566)

Coe, E.H.

Direct Submission

Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSU, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

Location/Qualifiers

1..2566

/organism="Zea mays"

/mol_type="mRNA"

/db_xref="MaizeDB:630315"

/db_xref="taxon:4577"

/clone_lib="Maize Mapping Project/DuPont Consensus Library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

BASE COUNT 440 a 680 c 777 g 420 t 249 others

ORIGIN

Alignment Scores:

Pred. NO.: 8.78e-167 Length: 2566

Score: 1557.00 Matches: 300

Percent Similarity: 75.46% Conservative: 69

Best Local Similarity: 61.35% Mismatches: 114

Query Match: 60.05% Indels: 7

DB: 11 Gaps: 1

US-09-848-806-1 (1-495) x AY109374 (1-2566)

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Db 688 CCGCAGGTGAAGCCCGTGTCCAGCCCGCGGTGCTGCTGGGGTGGGTGCGGCGCAAG 747

Qy 19 ThrProArgLeuArgAspHisTyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGly 38

Db 748 ACGGAGAACCTCAAGGACAAAGTACNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTTCGCG 807

Qy 39 ThrThrTyrLeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIlePro 58

Db 808 ACGACGACCTGTCGTGGAGCGCGCCACGGGAGGAGGAGTCCGCTGCAAGTGCATCTG 867

Qy 59 LysArgLysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMet 78

Db 868 AAGCCCAAGCTGGGCACGACGACGCTGGAGACGCTGCGCGGGAGATCCAGATAATG 927

Qy 79 HisHisLeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerVal 98

Db 928 CACCACCTGGCGGCCACCCACCGGTGTCGGCATCCGCGCGCGGTACGAGGACGCCGTG 997

Qy 99 PheValHisIleValMetGluValCysGluGlyGlyCyluLeuPheAspArgIleValSer 118

Db 988 GCGGTGCACCTCGTCATGGAGCTCTCGCGCGCGCGGAGCTGTTCACCGGATCGTGGC 1047

Qy 119 LysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValVal 138

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RESULT 3
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DEFINITION Zea mays CL1577_1 mRNA sequence.
ACCESSION  AY109401
VERSION     AY109401.1  GI:21213112
KEYWORDS    HTC.
SOURCE      Zea mays
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 2298)
AUTHORS     Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitesitt, M.S.,
            Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
TITLE       Maize Mapping Project/DuPont Consensus Sequences for Design of
            Overgo Probes
JOURNAL     Unpublished (2002)
REFERENCE   2 (bases 1 to 2298)
AUTHORS     Coe, E.H.
TITLE       Direct Submission
JOURNAL     Submitted (25-APR-2002) Maize Mapping Project, University of
            Missouri, Columbia, MO 65211, USA
COMMENT     If you are interested in getting corresponding physical clones,
            these are publicly available from ZmDB and may be found by BLAST
            searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
            www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
            maize cDNA sequences is either Virginia Walbot, Stanford or Pat
            Schnable, Iowa State, then clones may be requested from ZmDB:
            www.zmdb.iastate.edu.
FEATURES
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               Library"
               /note="this sequence is part of a project of EST
               assemblies resulting from the application of public
               contigs to seed DuPont contigs; this resource was
               assembled by DuPont as part of a collaboration for the
               overgo addressing of BACs in conjunction with the Maize
               Mapping Project"
BASE COUNT  544 a 464 c 597 g 524 t 169 others
ORIGIN
Alignment Scores:
Pred. No.: 9.7e-156      Length: 2298
Score: 1460.00          Matches: 278
Percent Similarity: 76.46%      Conservative: 76
Best Local Similarity: 60.04%      Mismatches: 107
Query Match: 56.31%      Indels: 2
DB: 11      Gaps: 2

US-09-848-806-1 (1-495) x AY109401 (1-2298)

QY      5  ProAsnProArgArgPro---SerAsnThrValLeuProTyrGlnThrProArgLeuArg 23
Db      600 CCTGTGCGCGGAGCCAGCCGCGGACACGATCTTGGCAGCAGTACGAGGACGTGCGC 659

QY      24 AspHisTyrLeuLeuGlyLysLysLeuGlyGlnGlnPheGlyThrThrTyrLeuCys 43
Db      660 TCTGTCTACTCCCTCGGAGGAGGCTTGGCGGGCCAGTTCGGGGTGACATACCTCTGC 719

QY      44 ThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuVal 63
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QY      64 CysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMethHisLeuSerGlu 83
Db      780 AGCAAGGCAGACAGGAGGACATTCGAAGGGAGATCCAGATCATGACGACCTGTCTGGG 839

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QY      84 HisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleVal 103
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QY      104 MetGluValCysGluGlyGlyLeuPheAspArgIleValSerLysGlyHisPheSer 123
Db      900 ATGAGCTCTGCCGAGTGGGAGGCTTTCGATCGCATCATTCGCCAAGGGGCACATACACA 959

QY      124 GluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSer 143
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QY      144 LeuGlyValMethHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAsp 163
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QY      164 AspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyr 183
Db      1080 AATGCAATGCTCAAGGCCACTGATTTGGGCTTCGCTCTCATCGAAGAGGAAAGATG 1139

QY      184 LeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyr 203
Db      1140 TACAGGAGACATCTGGAAGTGCTTATATGTTGCGCTCAAGTCTTAAAGCGAGCTAT 1199

QY      204 GlyProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuSerGlyVal 223
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QY      224 ProProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeu 243
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QY      244 AspPheLysSerAspProTrpProThrIleSerGluAlaAlaLysAspLeuIleTyrLys 263
Db      1320 GACTTTGAAAGTCAACCTTGGCCATCAATTTCTGAGAGTGCTTAAGACTTGGTTAGAAAG 1379

QY      264 MetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCysHisProTrp 283
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QY      284 IleValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeu 303
Db      1440 CTCAGAGAAGGTGGAGGTGCATCTGATAAGCCTATCGACAGCTGCTGTTCTTCTAGATG 1499

QY      304 LysGlnPheSerGlnMethAsnLysLysLysMetAlaLeuArgValIleAlaGluArg 323
Db      1500 AAGCAGTTTCAGAGCAATGAATAAGCTGNNNNNGATGGCCCTAAAGGTTATTGCTCAAAAC 1559

QY      324 LeuSerGluGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAspThrAspAsn 343
Db      1560 CTTAACGAGAGAGATCAAGGGGCTTAAAGCAATGTTTCATGAACATGGACACAGACAAT 1619

QY      344 SerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGlySerGluLeu 363
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QY      364 MetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspHisGlyThrIle 383
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QY      384 AspTyrGlyGluPheLeuAlaThrLeuHisMetAsnLysMetGluArgGluGluIle 403
Db      1740 GACTATGTTGAGTTCACTACTGCCACAATGTCATAGACACAAGCTCGAAAGGGGACGAGCAT 1799

QY      404 LeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThrIleAspGlu 423
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QY      424 LeuGlnSerAlaCysThrGluPheGlyLeuCysAspThr---ProLeuAspAspMethIle 442
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Qy 443 LysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAlaMetMet 462
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Qy 463 ArgLysGly 465
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RESULT 4
AY109463/c 1628 bp mRNA linear HTC 17-OCT-2002
LOCUS AY109463
DEFINITION Zea mays CL10776_2 mRNA sequence.
ACCESSION AY109463
VERSION AY109463.1 GI:21213192
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1628)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
Unpublished (2002)
2 (bases 1 to 1628)
Coe,E.H.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSU, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
FEATURES
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Library"
/notes="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed DuPont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project."
BASE COUNT 393 a 408 c 350 g 424 t 53 others
ORIGIN

Alignment Scores:
Pred. No.: 8,59e-145 Length: 1628
Score: 1362.50 Matches: 251
Percent Similarity: 76.28% Conservative: 77
Best Local Similarity: 58.37% Mismatches: 101
Query Match: 52.55% Indels: 1
DB: 11 Gaps: 1

US-09-848-806-1 (1-495) x AY109463 (1-1628)

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Qy 55 LysSerIleProLysArgLysLeuValCysArgGluAspTyrGluAspValTrpArgGlu 74
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Qy 95 GluAspSerValPheValHisIleValMetGluValCysGluGlyGlyGluLeuPheAsp 114
Db 1435 GAGACAGGCACCTCGGTCAACCTTGTATGAGCTCTCGAGGGCGGGAGCTCTTCGAC 1376

Qy 115 ArgIleValSerLysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIle 134
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Qy 135 LeuGlyValValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysProGlu 154
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Qy 215 IleLeuTyrIleLeuLeuSerGlyValProPheThrPheGluThrGluSerGlyIle 234
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Qy 335 LeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAla 354
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Qy 415 GlySerGlyTyrIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeu--- 433
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Qy 434 CysAspThrProLeuAspAspMetIleLysGluIleAspLeuAspAsnAspGlyLysIle 453

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Db 415 GATCAAAACATATAAAAGAAATCATCTGCTGAAGTAGATACAGATCATGATGAAGAAT 356
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RESULT 5
Bg647837
LOCUS EST509456 HOGA Medicago truncatula cDNA clone phOGA-18E5 5' end,
DEFINITION mRNA sequence.
ACCESSION BG647837.1 GI:13782949
VERSION BG647837
KEYWORDS Medicago truncatula (barrel medic)
SOURCE Medicago truncatula
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
REFERENCE 1 (bases 1 to 835)
AUTHORS Hahn,M.G., Ojanen-Reuhs,T., Samac,D., Town,C.D., Van Aken,S.,
Utterback,T., Cho,J., and Fraser,C.M.
TITLE ESTs from roots of Medicago truncatula treated with
oligogalacturonides of DP 6-20
JOURNAL Unpublished
COMMENT Contact: Michael G. Hahn
Complex Carbohydrate Research Center
University of Georgia
220 Riverbend Road, Athens, GA 30602-4712, USA
Tel: 706-542-4457
Fax: 706-542-4412
Email: hahn@crc.uga.edu
G391443e TIGR sequence name: MTMCE27TK More information is
available at: www.medicago.org
Seq primer: SKmod (CTA GAA CTA gtc gat CC).
FEATURES
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/db_xref="taxon:3880"
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with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
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/clone_lib="HOGA"
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XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
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extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in SOLR cells."
BASE COUNT 230 a 137 c 210 g 258 t
ORIGIN
Alignment Scores:
Pred. No.: 5.17e-118 Length: 835
Score: 1125.00 Matches: 223
Percent Similarity: 87.77% Conservative: 21
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Query Match: 43.39% Indels: 2
DB: 10 Gaps: 0
US-09-848-806-1 (1-495) x BG647837 (1-835)
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Qy 134 IleLeuGlyValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysPro 153
Db 62 ATTGTTGAGGTTGTTGAAGCTTGTCATCTCTTGAGTTATGCACAGAGACCTTAACACT 121
Qy 154 GluAsnPheLeuPheAspSerProLysAspAspAlaLysLeuLysAlaThrAspPheGly 173
Db 122 GAGAAATTTTGTGTTGATTGCTGATGAAGATGCTCTCTCAAAACTATTGATTTTGGT 181
Qy 174 LeuSerValPheThrLysProGlyGlnThrLeuThrAspValValGlySerProThrTyr 193
Db 182 TTGCTGTGTTTTTCAAGCCAGGTGAATCTTTAGTGATGTTGTTGGAAGCCCACTACTAT 241
Qy 194 ValAlaProGluValLeuLysLysCysTyrGlyProGluIleAspValTTPSerAlaGly 213
Db 242 GTTCGCCAGAGGCTTTCACAAACATTATGACCTGTAAGCAGACGTGTGGAGTCTCGT 301
Qy 214 VallLeuThrIleLeuLeuSerGlyValProProPheThrAlaGluThrGluSerGly 233
Db 302 GTTATTTGTACATCTTATTAAAGCGGGTGCCTCCGTTTTCGGCCGAGACCCATCAAGGG 361
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Db 542 CCTCTTGATTCTGCTGTTTTATCTCGCCTGAAGCAGATTCTCTGCGATGAATAAATCTAAA 601
Qy 314 LysMetAlaLeuArgValIleAlaGluArgLeuSerGluGluGluIleGlyGlyLeuLys 333
Db 602 AAGATGCTTTACGTGTTATTGCGGAGAGGCTTCTCGAGGAGAAATTTGGTGTGTTGAG 661
Qy 334 GluLeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLys 353
Db 662 GAGTTATTTCAGGATGCTTGATGCTGTAATAGTGAACATAACATTGGGAGAGTTAAAA 721
Qy 354 AlaGlyLeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAsp 373
Db 722 GAAGGCTTAAAGCGAGTAGGATCTGAACCTTATGGAGTCTGAATC-AAAGGATCTTTATGGAT 780
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Bg887873
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DEFINITION mRNA sequence.
ACCESSION BG887873
VERSION BG887873.1 GI:14264959
KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 814)
AUTHORS van der Hoeven,R., Bezzerides,J., Ewing,E., Cho,J., Chlemingo,A.,
Bougri,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.
TITLE Generations of ESTs from dormant potato tubers
JOURNAL Unpublished
COMMENT Contact: Robin Buell
The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@igr.org

This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:

http://genome.arizona.edu/orders/

Seq primer: M13F-R.

FEATURES

Location/Qualifiers

1..814
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/dev_stage="one month post-harvest"
/lab_host="SOLR"
/clone_lib="cSTD"

/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 40C. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tanksley lab notebooks."

BASE COUNT

242 a 146 c 191 g 235 t

ORIGIN

Alignment Scores:
Pred. No.: 8 43e-118 Length: 814
Score: 1123.00 Matches: 215
Percent Similarity: 90.0% Conservative: 30
Best Local Similarity: 79.04% Mismatches: 26
Query Match: 43.31% Indels: 2
DB: 12 Gaps: 0

US-09-848-806-1 (1-495) x BG887873 (1-814)

QY 125 ArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeu 144
DB 2 AGAAAAGCTGCACAAATTGATGAAACTATTGTCAAAGTTGTGGAGGCTTGCTATCTCT 61
QY 145 GlyValMetHisArgAspLeuLysProGluAanPheLeuPheAspSerProLysAspAsp 164
DB 62 GGGGTTATGCTAGAGATCTCAACCTGAGAAATTTCTTTTGTAGCTCTGATGAAGAT 121
QY 165 AlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeu 184
DB 122 GCTAAGCTTAAGCTACTGATTTGGTCTCTATTTCTTAAGCCAGGCGAGTATTTC 181
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QY 205 ProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValPro 224
DB 242 CCTGAAATAGAGCTCTGGAGTCTGGAGTCATCCCTTTATATCTCTTATGTTGGGTTCT 301
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QY 285 ValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLys 304
DB 482 GTGGATGATAATGTTGCTCCAGACAGGCCCTTGGTCTCTGACAGTTTGTCCGCCCTAAG 541

QY 305 GlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAlaGluArgLeu 324
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QY 365 GluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGlyThrIleAsp 384
DB 722 GAGTCGGAATCAAGCCTTGATGAGCGCGCTTGACTTTTGACACACAC-GGCATATCGAC 780
QY 385 Tyr-GlyGluPheLeuAlaAlaThrLeuHisMet 395
DB 781 TATGGTGAAATTCATCGCTGCAACATTTGCATTG 814

RESULT 7

CC331661/c

LOCUS

DEFINITION

CC331661

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Zeae mays

Zeae mays

REFERENCE

AUTHORS

.TITLE

JOURNAL

COMMENT

Unpublished

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@cigr.org

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

1..882

/organism="Zeae mays"

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BASE COUNT 129 a 316 c 271 g 166 t

ORIGIN

Alignment Scores:

Pred. No.: 8 55e-114 Length: 882

Score: 1088.50 Matches: 206

Percent Similarity: 82.94% Conservative: 37

Best Local Similarity: 70.31% Mismatches: 49

Query Match: 41.98% Indels: 1

DB: 29 Gaps: 1

US-09-848-806-1 (1-495) x CC331661 (1-882)

QY 132 LysThrIleLeuGlyValValGluAlaCysHisSerLeuGlyValMetHisArgAspLeu 151


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QY 167 LeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyrAsp 186
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Db 481 CTTAAGCCACAGTATTTGGTCTCTCCGTTTCTACACGACGAGTGAATGTTTCCGAT 540
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QY 187 ValValGlySerProTyrTyrValAlaProGluValLeuLysCysTyrGlyProGlu 206
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Db 541 GTGGTTGGAAGTCCTTACTATGTTGACCTGAGTTTACGCAAGCATATGACCTGAA 600
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QY 207 IleAspValTrpSerAlaGlyValIleLeuTyrIleLeuSerGlyValProPhe 226
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Db 601 TCTGATGTTGAGCGCAGGAGTATTTTGTACATATTACTTAGTGGCGTTCCACCTTT 660
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QY 227 TrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnCysLeuAspPheLys 246
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Db 661 TGGCGAAGAACCTGAGATGGAATATTTCCGCCAGATATTCAGCAAAATAGATTGAA 720
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QY 247 SerAspProTrpPro 251
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Db 721 ATCTGACCATGGCCT 735
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RESULT 9
BU302783
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BU302783 697 bp mRNA linear EST 09-APR-2002
aestivum cDNA clone whyd16m09 5', mRNA sequence.

BU302783.1 GI:20113529
EST.
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 697)
Ogiwara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished
Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..697
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/cultivar="Chinese Spring"
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BASE COUNT 139 a 200 c 194 g 164 t
ORIGIN

Alignment Scores:
Pred. No.: 4.56e-105 Length: 697
Score: 1011.00 Matches: 182
Percent Similarity: 90.7% Conservative: 24
Best Local Similarity: 80.1% Mismatches: 21
Query Match: 38.9% Indels: 0
DB: 12 Gaps: 0

US-09-848-806-1 (1-495) x BU302783 (1-697)

QY 61 LysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMethHis 80
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Db 15 AAGCTGCTGTCGCCGACGACTACGAGGACGTCCTGGCGGAGATCCAGATATGACAC 74
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QY 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100
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Db 75 CTCTCCGACGACCCCAACGTCGTCCGATCCGTGGCGCCTACGAGGACGCGCTCTTCGTG 134
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QY 101 HisIleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGly 120
|||
Db 135 CACATTGTCTATGAGGTCTGCCCGCGGGAGCTCTTCGACCGCATCTGCGCCAGGGG 194
|||
QY 121 HisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAla 140
|||
Db 195 CACTACACCGAGCGTCCGCGCAGCTCATCAGGACGATCGTTGGGGTCGTAGAGGCA 254
|||
QY 141 CysHisSerLeuGlyValMethHisArgAspLeuLysProGluAsnPheLeuPheAspSer 160
|||
Db 255 TGCACCTCCTCGCGTCTATGACCGGACCTCAAGCGGAGAACTTCCTGTTTGGCAGC 314
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QY 161 ProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysPro 180
|||
Db 315 ACTGCCGAGGACGCCCACTCAAGACTACCGATTTTCGGGTATTCATGTTCTACAGCCC 374
|||
QY 181 GlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLys 200
|||
Db 375 GGTGACAAATCTCTGATGTTGTTGGAGCCCCCTACTATGTTGCACCTGAGGTCTTCAG 434
|||
QY 201 LysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeu 220
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Db 435 AAATGCTATGTTCCAGAGCTGATGTCGAGTCTGGAGTCTGAGGAGTCTTCAGACAGATCTTCGA 494
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QY 221 SerGlyValProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGln 240
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Db 495 TGTGGCGTCCCCCTTCTGGCGCAGAACTGAAGCAGGAATCTTCAGACAGATCTTCGA 554
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QY 241 GlyLysLeuAspPheLysSerAspProTrpProThrIleSerGluAlaLysAspLeu 260
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Db 555 GGCACAACTGATTTTGGTCTGAGCCTGGCCTAGTATCTCTGACACGCGTAAAGATCTA 614
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QY 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerGluAlaLysLeuCys 280
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Db 675 CACCCATGATTTGTTGATGAT 695
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RESULT 10
BU990683
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BU990683 777 bp mRNA linear EST 21-AUG-2002
QGF20N08.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
QGF20N08, mRNA sequence.

BU990683
BU990683.1 GI:22410218
EST.
Lactuca sativa
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 777)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison
, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belong to contig QG_CA_Contig3691, see http://cgdb.ucdavis.edu/
for details.

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D	b		661	CTCAAGAAAATGGCTCTTAGGGTTATAGCGGAGAGCTTATCGAGAACAATA-GCTGGG	719
Q	y		332	LeuLysGluLeuPhelysMethIleAspThrAspAsnSerGlyThrIleThrPheGlu	350
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LOCUS					
DEFINITION					
EST389610 KV2 Medicago truncatula cDNA clone pkV2-22II11, mRNA					
sequence.					
ACCESSION					
BM779035					
VERSION					
BM779035.1 GI:19108729					
KEYWORDS					
EST,					
Medicago truncatula (barrel medic)					

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
 Medicago.
 1 (bases 1 to 813)
 Vandenbosch, K., Endre, G., Hur, J., Beremand, P., Town, C.D., Van Aken
 S., Uterback, T., Cheung, P., Tsai, J., and Fraser, C.M.
 2013.

JOURNAL
Sinorhizobium meliloti
Unpublished

CONTACT	COMMENT
Contact: VandenBosch K Department of Plant Biology University of Minnesota 220 Biosci Center 1495	Cartney Ave St Paul MN 55106

Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@cs.umn.edu
TICP kvandenb@cs.umn.edu
TICP kvandenb@cs.umn.edu

www.medicago.org
Seq primer: SKmod (CTA GAA CTA gtg gat CC) .
Location/Qualifiers
1 813
FEATURES
source

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/dev stage="2 days post-inoculation with Sinorhizobium
maliTori"
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/clone_lib="KV2"
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XhoI; cDNA was prepared from polyA+ enriched RNA
with
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cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack II Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using

BASE COUNT	ORIGIN	229 a	EX-assist	151 c	188 g	245 t	propagated in SOLR cells."

Argument scores:	
Pred. No.:	6.36e-102
Score:	984.50
Percent Similarity:	83.40%
Length:	813
Matches:	191
Conservative:	20

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Best Local Similarity: 75.49%      Mismatches: 40
Query Match:          37.97%      Indels:       3
DB:                   12           Gaps:        1
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QY 266 GluArgSerProLysLysArgIleSerAlaHisGluAlaLysHisProThrIleVal 285
 Db 421 GATAGGAATCCAAAGAGAGGTTAACTGCCCATGAAGTTTGTGCCATCGTGATCGTG 480

QY 286 AspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGln 305
 Db 481 GATGACTCAATGACCCCTGATAACCTTCTTGATTCGAGTTCTTCCACCCCTCAAGCAA 540

QY 306 PheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAlaGluArgLeuSer 325
 Db 541 TTCTCAGCAATGAACAACTAAAGAAATGGCTTTGGCTGTGATTGCCGAGAGCGCTATCA 600

QY 326 GluGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAspThrAspAsnSerGly 345
 Db 601 GAAGAGGAGATTGGTGGCCTCAAGGAGCTATTCAAAATGTTAGACACAGACAATAGTGA 660

QY 346 ThrIleThrPheGluGluLeuLys 353
 Db 661 AACATAACCTTTTCAGAACTAAAA 684

RESULT 13

BQ865474 751 bp mRNA linear EST 14-AUG-2002
 LOCUS QGC5A16.vg.ab1 QG_ABCDI lettuce salinas Lactuca sativa cDNA clone
 DEFINITION QGC5A16 mRNA sequence.

ACCESSION BQ865474
 VERSION BQ865474.1 GI:22250939
 KEYWORDS EST.

SOURCE

ORGANISM Lactuca sativa
 Lactuca sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
 Cichorieae; Lactuca.

REFERENCE

AUTHORS Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison
 P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
 Church, S., Jackson, L. and Bradford, K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
 http://comgenomics.ucdavis.edu/
 Unpublished

JOURNAL

COMMENT Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmunsdon Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
 belongs to contig QG_CA_Config3691, see http://cgdb.ucdavis.edu/
 for details.
 Plate: QGC5 row: A column: 16.

FEATURES

source

1..751
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 from 10 different sources of RNA from a single genotype.
 Separate cDNAs were generated using primers that
 incorporated unique 5' and 3' tags to distinguish each
 source of RNA. cDNAs were then pooled, size-fractionated,
 directionally cloned into a custom medium-copy vector and
 transformations made with four size classes to minimize

size bias. Details of each source of RNA and library
 construction can be obtained at http://cgdb.ucdavis.edu/
 TAG_LIB=QG_ABCDI lettuce salinas
 TAG_TISSUE=chemical induction
 TAG_SEQ=TTGTAGCCGGG"

BASE COUNT 218 a 117 c 180 g 236 t
 ORIGIN

Alignment Scores:

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 Best Local Similarity: 71.60% Mismatches: 40
 Query Match: 37.06% Indels: 1
 DB: 13 Gaps: 0

US-09-848-806-1 (1-495) x BQ865474 (1-751)

QY 75 IleGlnIleMetHisHisLeuSerGluHisProAsnValValArgIleLysGlyThrTyr 94
 Db 3 ATTACATAATGCATCATTTAGCAGGCGCATCCGAATGTTATAGCCATTAAGAGGCTTAT 62

QY 95 GluAspSerValPheValHisIleValMetGluValCysGluGlyGlyGluLeuPheAsp 114
 Db 63 GAAGATGCTGTTGCAGTTCATGTTGTTATGGAATATTGTGCAGGAGGTGAGCTTTTGTAT 122

QY 115 ArgIleValSerLysGlyHisPheSerGluArgGluAlaValLysLysLysIleThrIle 134
 Db 123 AGGATTTATTTCAAGAGAGGACATTACACTGAAAAAAGACGACGTTCAGCTTACAAAGCATT 182

QY 135 LeuGlyValValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysProGlu 154
 Db 183 GTTGGGTTTGTGGAGACTTGTCTCTTTAGGGGTTATGCATCGCATTTAAAGCCCTGAA 242

QY 155 AsnPheLeuPheAspSerProLysAspAspAlaLysLeuLysAlaThrAspPheGlyLeu 174
 Db 243 AATTTCTTCTGTTGTTGATAAGAAAGAAAGATTGCTCTCTCAAAACTATTGATTGGAATTA 302

QY 175 SerValPheTyLysProGlyGlnTyLysLeuTyLysAspValValGlySerProTyLysVal 194
 Db 303 TCGGTTTTCTTCAAAACCGGTGAATCATTAATGATGTGGTTGGAAGCCCATATTATGTT 362

QY 195 AlaProGluValLeuLysLysCysTyLysGlyProGluIleAspValTrpSerAlaGlyVal 214
 Db 363 GCACACAGAAGTTTTCAGAAAACGTTATGCGCTTGAAGCAGACGTTTGGAGTGTGGGTT 422

QY 215 IleLeuTyLysLeuLeuSerGlyValProPheTrpAlaGluThrGluSerGlyIle 234
 Db 423 ATTGTTTATATCTTAAAGTGGTGTACCTCCATTTTGGCTGAAACGGAGCAAGGAATA 482

QY 235 PheArgGlnIleLeuGlnGlyLysLeuAspPheLysSerAspProTrpProThrIleSer 254
 Db 483 TTGGAACAAGTCTCTCAAGGCGATCTTGATTTCTCTTCATGATCCATGGCCCAATATTTCT 542

QY 255 GluAlaAlaLysAspLeuIleTyLysMetLeuGluArgSerProLysLysArgIleSer 274
 Db 543 GAAGATGCAAAAAGATCTTGTAAAGGAGATGCTTATTTCGAGACCTTAAAGACGATTAACT 602

QY 275 AlaHisGluAlaLeuLysHisProTrpIleValAspGluGlnAlaAlaProAspLysPro 294
 Db 603 GCACATGAAGTTTATGTCATCTTGGGTTCAAGTTGATGGCTGGCTCCAGACCAAGCCT 662

QY 295 LeuAspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLys 314
 Db 663 CTCGACTCTGCAAGTCTTAAGTAGAATGAA-CAATTTTCAGCCATGAATAAGCTTTAGAAA 721

QY 315 MetAlaLeuArgValIleAlaGluArgLeu 324
 Db 722 ATGGCTTTGAGGGTTATAGCTGAGAGTATG 751

RESULT 14

CB677374

LOCUS

827 bp mRNA linear EST 09-APR-2003

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 28, 2003, 10:44:32 ; Search time 96 Seconds

(without alignments)
2275.882 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRPSNTVLPQTP.....KMLNFIADAFVDEKSD 495

Scoring table:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1277.5	49.3	1349	4	US-08-459-504B-20
5	1277.5	49.3	1349	5	US-08-459-444-20
6	1277.5	49.3	1349	6	US-09-547-422-20
7	1159.5	44.7	4162	2	US-08-459-448A-26
8	1159.5	44.7	4162	3	US-08-459-595A-26
9	1159.5	44.7	4162	3	US-08-459-504B-26
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13	831	32.0	2374	3	US-09-347-801-3	Sequence 3, Appli
14	771.5	29.8	1400	1	US-08-464-164-1	Sequence 1, Appli
15	771.5	29.8	1400	1	US-08-338-057-1	Sequence 1, Appli
16	771.5	29.8	1400	2	US-08-668-416-1	Sequence 1, Appli
17	623	24.0	2514	3	US-08-655-352-1	Sequence 1, Appli
18	623	24.0	2514	4	US-09-258-016-1	Sequence 1, Appli
19	623	24.0	2514	4	US-09-257-825B-1	Sequence 1, Appli
20	587.5	22.7	1480	4	US-09-016-434-1454	Sequence 1454, Ap
21	582	22.4	1776	3	US-08-655-352-10	Sequence 10, Appl
22	582	22.4	1776	4	US-09-258-016-10	Sequence 10, Appl
23	582	22.4	1776	4	US-09-257-825B-10	Sequence 10, Appl
24	561.5	21.7	1733	4	US-09-620-312D-526	Sequence 526, App
25	558.5	21.5	1694	4	US-09-579-664B-3	Sequence 3, Appli
26	543	20.9	2061	4	US-09-800-960-1	Sequence 1, Appli
27	536	20.7	1282	3	US-08-878-989-12	Sequence 12, Appl
28	536	20.7	1282	3	US-09-272-796-12	Sequence 12, Appl
29	536	20.7	1282	4	US-09-016-434-953	Sequence 953, App
30	535.5	20.7	3471	2	US-08-715-568A-2	Sequence 2, Appli
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32	501	19.3	2298	4	US-09-975-326-3	Sequence 3, Appli
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34	491	18.9	4935	2	US-08-631-097-3	Sequence 3, Appli
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36	489.5	18.9	2132	2	US-09-159-385-3	Sequence 3, Appli
37	489.5	18.9	2132	3	US-09-186-277-3	Sequence 3, Appli
38	482.5	18.6	1429	2	US-09-159-385-4	Sequence 4, Appli
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40	479.5	18.5	1929	4	US-09-359-161-4	Sequence 4, Appli
41	476	18.4	1735	4	US-09-746-694-3	Sequence 3, Appli
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44	459.5	17.7	2934	1	US-08-198-446B-16	Sequence 16, Appl
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ALIGNMENTS

RESULT 1

US-07-951-715A-20
; Sequence 20, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlino, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO. 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1349 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..1226
; OTHER INFORMATION: /note= "cDNA sequence for maize
; OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
; OTHER INFORMATION: disclosed in Figure 30."
; US-07-951-715A-20

Alignment Scores:
Pred. No.: 3,16e-132 Length: 1349
Score: 1277.50 Matches: 242
Percent Similarity: 76.98% Conservative: 59
Best Local Similarity: 61.89% Mismatches: 89
Query Match: 49.27% Indels: 1
DB: 1 Gaps: 1

US-09-848-806-1 (1-495) x US-07-951-715A-20 (1-1349)

QY 76 GluileMethHisHisLeuSerGluHisProAsnValValArgileLysGlyThrTyrGlu 95
DB 3 CAGATCATGACCACCTCTCCGGCCAGCCCAACAGCTGGTGGGCGCTCCGGCGCGGTACGAG 62
QY 96 AspSerValPheValHisIleValMetGluValCysGluGlyGlyGluLeuPheAspArg 115
DB 63 GACAAGCAGAGCGTGCACCTCGTCATGGAGCTGTGCGGCGCGGGAGCTCTTCGACCGC 122
QY 116 IleValSerLysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeu 135
DB 123 ATCATCGCGCGGGCCAGTACAGCGAGCGCGCGCGCGCGAGCTGTGCGCGCCATCGTG 182
QY 136 GlyValValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsn 155
DB 183 CAGATCGTGACACCTGCGCACTCCATGGGGGTGATGACCGGACATCAAGCCCGAGAAC 242
QY 156 PheLeuPheAspSerProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSer 175
DB 243 TTCCTGCTGCTCAGCAAGGACGAGGAGCGCGCTCAAGGCCACCGACTTCGGCCCTCC 302
QY 176 ValPheTyrLysProGlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAla 195
DB 303 GTCTCTTCAAGGAGGCGCGCTGCTCAGGGACATGCTCGGACGCGCTACTACATCGCG 362
QY 196 ProGluValLeuLysCysTyrGlyProGluLeuAspValTrpSerAlaGlyValIle 215
DB 363 CCGGAGGTCTCAAGAGGAGTACGGCCCGGAGCGGACATCTGGAGCGTCTGGCGTCATG 422
QY 216 LeuTyrIleLeuLeuSerGlyValProPheTrpAlaGluThrGluSerGlyIlePhe 235
DB 423 CTCATCATCTTCCTCGCGCGGTCTCTCTCTGCGGACAGAACGAGACGCGCATCTTC 482
QY 236 ArgGlnIleLeuGlnGlyLysLeuAspPheLysSerAspProTrpProThrIleSerGlu 255
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Db 483 ACCGCCATCTCGGAGGCGAGCTTGACCTCTCAGGCGGAGCATGGCCACACATCTCCCGC 542
QY 256 AlaAlaLysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAla 275
Db 543 GGAGCCCAAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGCG 602
QY 276 HisGluAlaLeuCysHisProTrpIleValAspGluGlnAlaProAspLysProLeu 295
Db 603 TTCAGGTCTCTCAATCACCCTATGGATCAAGAAGACGCGGAGCGCTCACGCGCGCTT 662
QY 296 AspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMet 315
Db 663 GACAACGTTGTTCTCGACAGGCTCAAGCAGTTTCAGGCCCATGAACCAAGTTCAAGAAGCA 722
QY 316 AlaLeuArgValIleAlaGluArgLeuSerGluGluIleGlyGlyLeuLysGluLeu 335
Db 723 GCATTGAGGATCATAGCTGGGTGCTTATCGAAGAGGAGATCACAGGGCTGAAGGAGATG 782
QY 336 PheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGly 355
Db 783 TTCAGAACAATTGACCAAGGATAACAGCGGACCATTTACCTCGACGAGCTCAACACCGG 842
QY 356 LeuLysArgValGlySerGluLeuMetGluSerGluLysSerLeuMetAspAlaAla 375
Db 843 TTGCGCAAGCAGCGGCCCAAGCTGTCTCAGCAGCGGAAATGGAGAACTAATGGAGCAGCT 902
QY 376 AspIleAspAsnSerGlyThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHisMet 395
Db 903 GACGCTGACGGCAACGGGTAAATTGACTACGCAATTCGTACCGCAACAGTGCATATG 962
QY 396 AsnLysMetGluArgGluGluLeuValAlaAlaPheSerAspPheAspLysAspGly 415
Db 963 AACAAATCGATAGAGAGAGACACCTTTACACAGCATTCAGTATTTGCAAGGAGCAAC 1022
QY 416 SerGlyTyrIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAsp 435
Db 1023 AGCGGTACTACTAAAGAGAGCTTGACGCGCTTGAGGAGGACAGGTTGTATGAC 1082
QY 436 Thr---ProLeuAspAspMetIleLysGluIleAspLeuAspAsnAspGlyLysIleAsp 454
Db 1083 GCGGATAAAATCAAGACATCATCTCCGATGCGGACTCTGACAATGATGAAGGATAGAT 1142
QY 455 PheSerGluPheThrAlaMetMetArgLysGly 465
Db 1143 TATTCAGAGTTTGTGCGCATGATGAGGAAAGG 1175
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RESULT 2

US-08-459-48A-20
; Sequence 20, Application US/08459448A
; Patent No. 5859336

GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttle, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation

STREET: Patent & Trademark Dept., 520 White Plains

STREET: Rd., POB 2005

CITY: Tarrytown

STATE: New York

COUNTRY: USA

ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,448A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA: US 07/772,027

APPLICATION NUMBER: 04-OCT-1991

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.

REGISTRATION NUMBER: 40403

REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8582

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

OTHER INFORMATION: /note= "cDNA sequence for maize

OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as

OTHER INFORMATION: disclosed in Figure 30."

US-08-459-448A-20

Alignment Scores:

Pred. No.: 3.16e-132 Length: 1349

Score: 1277.50 Matches: 242

Percent Similarity: 76.98% Conservative: 59

Best Local Similarity: 61.89% Mismatches: 89

Query Match: 49.27% Indels: 1

DB: 2 Gaps: 1

US-09-848-806-1 (1-495) x US-08-459-448A-20 (1-1349)

QY 76 GlnIleMetHisLeuSerGluHisProAsnValValArgIleLysGlyThrTyrGlu 95
 Db 3 CAGATCATGCACACCTCTCCGCCAGCCACCTGTGGGCTCCCGCGCGGTACGAG 62
 QY 96 AspSerValPheValHisIleValMetGluValCysGluGlyGlyGluLeuPheAspArg 115
 Db 63 GACAAGCAGAGGCTGCACCTCGTCATGAGCTGTGGCGCGCGGAGCTCTTCGACCG 122
 QY 116 IleValSerLysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeu 135
 Db 123 ATCATCGCCCGGCGCAGTACACGGAGCGCGCGGCTGTGGCGGCCCATCGTG 182
 QY 136 GlyValValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysProGluAen 155
 Db 183 CAGATCGTGCACACCTGCCACTCCATCGGGGTGTGTCACCGGACATCAAGCCCGAGAAC 242
 QY 156 PheLeuPheAspSerProLysAspAspAlaLysLeuLysAlaThrAspPheGlyLeuSer 175
 Db 243 TTCCTGCTCTCAGCAAGGACGAGGACGCGCGCTCAAGGCCACCGACTTCGGCCTCTCC 302

QY 176 ValPheTyrLysProGlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAla 195
 Db 303 GTCTTCTCAAGGAGGCGAGCTGCTCAGGACATCGTCGGCAGCGCTACTACATCGCG 362
 QY 196 ProGluValLeuLysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIle 215
 Db 363 CCGAGGTGCTCAAGAGGAGTACGGCCCGGAGCGGACATCTGGAGCGTGGCGTCATG 422
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 Db 423 CTCATCATCTTCTCGCGCGGTGCTCTCTTGGCAGAGAACGAGAACCGCATCTTC 482
 QY 236 ArgGlnIleLeuGlnGlyLysLeuAspPheLysSerAspProTrpThrIleSerGlu 255
 Db 483 ACGCCATCTCGAGGCGAGCTTGACCTCTCCAGCGAGCCATGGCCACATCTCGCG 542
 QY 256 AlaAlaLysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAla 275
 Db 543 GGAGCCCAAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGGAGCGCTCACGCG 602
 QY 276 HisGluAlaLeuCysHisProTrpIleValAspGluGlnAlaAlaProAspLysProLeu 295
 Db 603 TTCAGGTCTCAATCACCCTGATCAAGAGACGGAGACCGGCTTGACCGCGCTT 662
 QY 296 AspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMet 315
 Db 663 GACAACGTTGTTCTCGACAGGCTCAAGCAGTTTCAGGCGCCATGAACAGTTCAAGAAAGCA 722
 QY 316 AlaLeuArgValIleAlaGluArgLeuSerGluGluGluIleGlyLeuLysGluLeu 335
 Db 723 GCATTGAGGATCATAGCTGGGTGCTTATCCGAAGAGGAGATCACAGGCTGAAGGAGATG 782
 QY 336 PheLysMetIleAspThrAspAsnSerGlyThrIlePheGluGluLeuLysAlaGly 355
 Db 783 TTCAGAACATTCAGCAAGGATTAACAGCGGACCATTTACCTCCAGGAGCTCAACACCGG 842
 QY 356 LeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAla 375
 Db 843 TTGGCAAGCAGCGGCCCAAGCTGTTCAGACAGCGAAATGGAGAACTAATGGAAGCAGCT 902
 QY 376 AspIleAspAsnSerGlyThrIleAspTyrGlyPheLeuAlaAlaThrLeuHisMet 395
 Db 903 GACGCTGACGGCAACGGGTAAATTGACTACGAGCAATTCGTACCCGCAACAGTGCATATG 962
 QY 396 AsnLysMetGluArgGluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGly 415
 Db 963 AACAACTCGATAGAGAGACGACCTTTACACAGCAATTCAGTATTTCGACAAAGCAAC 1022
 QY 416 SerGlyTyrIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAsp 435
 Db 1023 AGCGGTACATTACTAAAGAGAGCTTGAGCAGCGCTTGAAGGAGCAAGGTTGTATGAC 1082
 QY 436 Thr---ProLeuAspAspMetIleLysGluIleAspLeuAspAsnAspGlyLysIleAsp 454
 Db 1083 GCCGATAAAATCAAGACATCATCTCCGATCGCGACTCTGCACAATGATGAAGGATAGAT 1142
 QY 455 PheSerGluPheThrAlaMetMetArgLysGly 465
 Db 1143 TATTGAGATTGTGGCGATGATGAGAAAGGG 1175

RESULT 3

US-08-459-595A-20

; Sequence 20, Application US/08459595A

; Patent No. 6018104

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; APPLICANT: Desai, Nallini M.

; APPLICANT: Lewis, Kelly S.

; APPLICANT: Kramer, Vance C.

; APPLICANT: Warren, Gregory W.

; APPLICANT: Evola, Stephen V.

; APPLICANT: Crossland, Lyle D.

Db 1143 TATTGAGAGTTTGTGGCGATGATGAGAAAGGG 1175

RESULT 4

US-08-459-504B-20

Sequence 20, Application US/08459504B

Patent No. 6075185

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.

APPLICANT: Kramer, Vance C.

APPLICANT: Warren, Gregory W.

APPLICANT: Evola, Stephen V.

APPLICANT: Crossland, Lyle D.

APPLICANT: Wright, Martha S.

APPLICANT: Merlin, Ellis J.

APPLICANT: Launis, Karen L.

APPLICANT: Rothstein, Steven J.

APPLICANT: Bowman, Cindy G.

APPLICANT: Dawson, John L.

APPLICANT: Dunder, Erik M.

APPLICANT: Pace, Gary M.

APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6075185artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,504B

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/459,595

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

OTHER INFORMATION: /note= "cDNA sequence for maize pollen-specific calcium dependent protein kinase gene as disclosed in Figure 30."

OTHER INFORMATION: disclosed in Figure 30."

US-08-459-504B-20

Alignment Scores:

Pred. No.: 3.16e-132 Length: 1349

Score: 1277.50 Matches: 242

Percent Similarity: 76.98% Conservative: 59

Best Local Similarity: 61.89% Mismatches: 89

Query Match: 49.27% Indels: 1

DB: 3 Gaps: 1

US-09-848-806-1 (1-495) x US-08-459-504B-20 (1-1349)

QY 76 GlnIleMetHisHisLeuSerGluHisProAsnValValArgIleLysGlyThrTyrGlu 95

Db 3 CAGATCATGCACCACTCTCCGGCCAGCCCAACGTGGTGGGCTCCGGCGCGTACGAG 62

QY 96 AspSerValPheValHisIleValMetGluValCysGluGlyGlyGluLeuPheAspArg 115

Db 63 GACAAGCAGAGCGGTGCACCTGTCATGAGCTGTCCGGGGGGGGAGCTCTTCACCCG 122

QY 116 IleValSerLysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeu 135

Db 123 ATCATCGCCCGGGCCAGTACACGAGCGCGCGCGCGGAGCTCTGCGGCCCATCGTG 182

QY 136 GlyValValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsn 155

Db 183 CAGATCGTGCACCTGCCACTCTCCATGGGGGTGATGCACCGGACATCAAGCCCGAGAAC 242

QY 156 PheLeuPheAspSerProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSer 175

Db 243 TTCTCTGCTGCTCAGCAAGGAGCGCGCGCTCAAGGCCACCGACTCTCGGCTCTCC 302

QY 176 ValPheTyrLysProGlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAla 195

Db 303 GTCTTCTTCAAGGAGGGCGAGCTGCTCAGGGACATCTGTCGCGCGCTACTTACATCGCG 362

QY 196 ProGluValLeuLysLysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIle 215

Db 363 CCCGAGGTGCTCAAGAGGAAGTACGGCCCGGAGCGGCACATCTGGAGGCTCGCGCTCATG 422

QY 216 LeuTyrIleLeuLeuSerGlyValProPheTrpAlaGluThrGluSerGlyIlePhe 235

Db 423 CTCTACATCTTCTCGCGGGGTGCTCTTCTGGGCGAGAGAACGAGAACGGCATCTTC 482

QY 236 ArgGlnIleLeuGlnGlyLysLeuAspPheLysSerAspProTrpProThrIleSerGlu 255

Db 483 ACCGCCATCTCGAGGGCGAGCTTTGACCTCTCCAGCGAGCCATGCGCCACATCTCGCG 542

QY 256 AlaAlaLysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAla 275

Db 543 GGAGCCCAAGGATCTGCTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGGCG 602

QY 276 HisGluAlaLeuCysHisProTyrIleValAspGluGlnAlaAlaProAspLysProLeu 295

Db 603 TTCAGGTCTCAATCACCCTCCATGGATCAAGAGACGGAGCGCGCTGACACGCCGCTT 662

QY 296 AspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMet 315

Db 663 GACAACGTTGTTCTCGACAGGCTCAAGCAGTTTCAGGGCCATGAACCATTTCAAGAAAGCA 722

QY 316 AlaLeuArgValIleAlaGluArgLeuSerGluGluIleGlyGlyLeuLysGluLeu 335

Db 723 GCATTGAGGATCATAGCTGGGTGCTTATCCGAAGGAGGATCACAGGCTGAAGGAGATG 782

QY 336 PheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGly 355

Db 783 TTCAGAAACATTGACAGGATTAACAGCGGGGACCATTTACCTCTGACGAGCTCAACACCGGG 842

QY 356 LeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAla 375

Db 843 TTGCAAAAGCAGCGGCCCAAGCTGTTCAGACAGCGAAATGGAGAACTAATGGAAGCAGCT 902

QY 376 AspIleAspAsnSerGlyThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHiMet 395

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Db 843 TTGCAAGACGCGCCCAAGCTGTTCAGACAGCGAAATGGAGAACTAATGGAAGCAGCT 902
Qy 376 AspileAspAsnSerGlyThrIleAspTyrGlyGluPheLeuAlaIleThrLeuHisMet 395
Db 903 GACGCTGACCGCAACGGGTTAATTGACTACAGCAATTCGTACCGCAACAGTGCATATG 962
Qy 396 AsnLysMetGluArgGluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGly 415
Db 963 AACAACTGGATAGAGAAGACCTTTACACAGCATTCAGTATTTTCGACAAAGGACAAC 1022
Qy 416 SerGlyTyrIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAsp 435
Db 1023 AGCGGGTACATTACTAAAGAGAGCTTGACGACCGCTTGAAGGAGCAAGGGTTGTATGAC 1082
Qy 436 Thr---ProLeuAspAspMetIleLysGluIleAspLeuAspAsnAspGlyLysIleAsp 454
Db 1083 GCCGATAAATCAAGACATCATCTCCGATGCCGACTCTGACATGATGGAAGATAGAT 1142
Qy 455 PheSerGluPheThrAlaMetMetArgLysGly 465
Db 1143 TATTTCAGAGTTTGTGGCGATGATGAGGAAAGGG 1175

RESULT 6

US-09-547-422-20
; Sequence 0, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Kosziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lytle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 'note="cDNA sequence for maize
; pollen-specific calcium dependent protein kinase gene as

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1349 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..1226
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-547-422-20
Alignment Scores:
Pred. No.: 3,16e-132 Length: 1349
Score: 1277.50 Matches: 242
Percent Similarity: 76.98% Conservative: 59
Best Local Similarity: 61.89% Mismatches: 89
Query Match: 49.27% Indels: 1
DB: 4 Gaps: 1

US-09-848-806-1 (1-495) x US-09-547-422-20 (1-1349)

Qy 76 GlnIleMetHisHisLeuSerGluHisProAsnValValArgIleLysGlyThrTyrGlu 95
Db 3 CAGATCATGCACCACTCTCCGGCCAGCCCAACAGTGTGGCCCTCCGGCGCGGTAGAG 62
Qy 96 AspSerValPheValHisIleValMetGluValCysGluGlyGlyGluLeuPheAspArg 115
Db 63 GACAAGCAGAGCGTGCACCTCGTCATGGAGCTGTGGCGGGGGAGCTCTTCGACCGC 122
Qy 116 IleValSerLysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeu 135
Db 123 ATCATCGCCGGGCGAGTACACGAGCGCGCGGAGCTGTGGCGCGCATCGTG 182
Qy 136 GlyValValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsn 155
Db 183 CAGATCGTCACACCTGCCACTCCATGGGGGTGATCCACCGGACATCAAGCCGAGAAC 242
Qy 156 PheLeuPheAspSerProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSer 175
Db 243 TTCTGCTCTCAGCAAGACGAGGACGCGCGCTCAAGGCCACCGACTTCGGCCTCTCC 302
Qy 176 ValPheTyrLysProGlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAla 195
Db 303 GTCTTCTTCAGAGGCGCGAGCTGTCTAGGGACATCGTCGCGAGCCCTACTACATCGCG 362
Qy 196 ProGluValLeuLysLysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIle 215
Db 363 CCGAGGTGCTCAAGAGGAAGTACGGCCCGGAGGCGGACATCTGGAGCGTCGGCGTCATG 422
Qy 216 LeuTyrIleLeuLeuSerGlyValProPheThrAlaGluThrGluSerGlyIlePhe 235
Db 423 CTCTACATCTCTCGCGCGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 482
Qy 236 ArgGlnIleLeuGlnGlyLysLeuAspPheLysSerAspProTyrProThrIleSerGlu 255
Db 483 ACGGCATCTCTCGAGGCGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 542
Qy 256 AlaAlaLysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAla 275
Db 543 GGAGCCAAAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGGCTCAGCGG 602
Qy 276 HisGluAlaLeuCysHisProTrpIleValAspGluGlnAlaAlaProAspLysProLeu 295
Db 603 TTCAGGTCCTCAATCACCCTATGATCAAGAAGACGAGGAGCGCGCTCTGACCGCGCTT 662
Qy 296 AspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMet 315
Db 663 GACAAGTGTGTCTCGACAGGCTCAAGCAGTTTCAGGGCGCATGAACACGAGTTCAAGAAGCA 722
Qy 316 AlaLeuArgValIleAlaGluArgLeuSerGluGluGluIleGlyLeuLysGluLeu 335

; disclosed in Figure 30."

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Db 783 TTCAAGAACATTTGCAAGGATAACAGCGGACCATTTACCTCGAGAGCTCAAAACACGGG 842
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Db 843 TTGCAAGACGCGGCCCAAGCTGTACAGACGCGAAATGGAGAACTAATGGAAGCAGCT 902
Qy 376 AspIleAspAsnSerGlyThrIleAspTyrglyGluPheLeuAlaLaThrLeuHisMet 395
Db 903 GACGCTGACGCGCAACGGGTAAATGACTACGACGAAATTCGTCACCGCAACAGTGCATATG 962
Qy 396 AsnLysMetGluArgGluGluIleuValalalaphSerAspPheAspLysAspGly 415
Db 963 AACAACTGGATAGAGAGACACCTTTACACAGCATTTCCAGATTTTCGACAAGGACAAC 1022
Qy 416 SerGlyTyrlleThrIleAspGluLeuGlnSerAlaCysThrGluPheGluLeuCysAsp 435
Db 1023 AGCGGTACATTACTAAGAGAGAGCTTGAGCAGCCTTGAAGGAGCAAGGGTTGTATGAC 1082
Qy 436 Thr----ProLeuAspAspMetIleLysGluIleAspLeuAspAsnAspGlyLysIleAsp 454
Db 1083 GCCGATAAAATCAAAGACATCATCTCCGATCCCGACTCTGACATGATGGAAGATAGAT 1142
Qy 455 PheSerGluPheThrAlaMetMetArgLysGly 465
Db 1143 TATTCAGAGTTTGTGGCGATGATGAGGAAGGG 1175

RESULT 7

US-08-459-448A-26
; Sequence 26, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1418..1427
; OTHER INFORMATION: /note= "start of mRNA"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1481..2366
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2367..2451
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2452..2602
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2603..2690
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2691..2804
; FEATURE:
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; LOCATION: 2805..2906
; FEATURE:
; NAME/KEY: exon
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; NAME/KEY: intron
; LOCATION: 3076..3177
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3178..3304
; FEATURE:
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; FEATURE:
; NAME/KEY: exon
; LOCATION: 3399..3498
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3499..3713
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3714..3811
; FEATURE:
; NAME/KEY: promoter
; LOCATION: 1..1477
; IDENTIFICATION METHOD: experimental
; OTHER INFORMATION: /partial
; OTHER INFORMATION: /function= "pollen-specific promoter region"
; OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-448A-26

Alignment Scores:

Pred. No.: 2,31e-118 Length: 4162
Score: 1159.50 Matches: 276
Percent Similarity: 50.00% Conservative: 69
Best Local Similarity: 40.00% Mismatches: 115
Query Match: 44.72% Indels: 235
DB: 2 Gaps: 7

US-09-848-806-1 (1-495) x US-08-459-448A-26 (1-4162)

QY 6 AsnProArgArgProSerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHis 25
DB 1698 AACCGCGCGCGCGTGG-GGCAGCGTGTGGCGCGCCCATGGAGAGCGTGGCGCGGACC 1756

QY 26 TyrLeuLeuGlyLysLysLeuGlyGlnGlnPheGlyThrThrTyrLeuCysThrGlu 45
DB 1757 TACTCGATGGCAAGAGCTCGGCGCGGCGAGTTCGGCGTGACGACCTGTGCACGCGAC 1816

QY 46 LysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArg 65
DB 1817 CGGACGCGCGCGAGAGTGGCGGTCAAGACGATCGCAAGCGGAGCTGGCGCGGACG 1876

QY 66 GluAspTyrGluAspValTyrArgGluIleGlnIleMetHisHisLeuSerGluHisPro 85
DB 1877 GAGGACGTGGACGCGTGGCGCGGAGGTGCAGATCATGCACCATCTTCGCGCCAGCCC 1936

QY 86 AsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleValMetGlu 105
DB 1937 AACGTGGTGGCGTCCGCGCGCGTACGAGGACAAGCAGCGTGCACCTCGTCATGGAG 1996

QY 106 ValCysGluGlyGlyLeuLeuPheAspArgIleValSerLysGlyHisPheSerGluArg 125
DB 1997 CTGTGGCGCGCGGCGAGCTTTCGACCGCATCATCGCGCGGCGCGAGTACACGAGCGC 2056

QY 126 GluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGly 145
DB 2057 GCGCGCGCGAGCTGTGGCGCGCATCTGCAGATCTGCACACCTGCCACTCCATGGGG 2116

QY 146 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAspAla 165
DB 2117 GTGATCACCGGACATCAAGCCCGAGAACTTCCTGCTGCAGCAAGGACGAGCGCG 2176

QY 166 LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr 185
DB 2177 CGGCTCAAGGCCACCGACTTCGGCCCTCTCCGCTCTTCTCAAGGAGGCGGCTGCTCAGG 2236

QY 186 AspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyrGlyPro 205
DB 2237 GACATCGTGGCAGCGCCTACTACATCGCGCGCGAGGTGCTCAAGAGGAAGTACGCGCG 2296

QY 206 GluIleAspValTyrSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValProPro 225
DB 2297 GAGGCGGACATGAGAGCGTGGCGTGCATGCTTACATCTTCTCGCGCGGCTGCTCC 2356

QY 226 PheTyrAla- 228
DB 2357 TTCTGGGC-AGGTGGATCGTCCGTTGCTGCTAGACGATATACAGAACCCGAGCATG 2415

QY 229 -----GluThrGluSerGlyIlePheArgGln 237
DB 2416 GATTTGCTTCTCAGCCCTGTTCTTGTCATCACCAGAGAACGAGACGTCATCTTCCCGCC 2475

QY 238 IleLeuGlnGlyLysLeuAspPheLysSerAspProTyrProThrIleSerGluAlaAla 257
DB 2476 ATCCCTGCGAGGCGAGCTGACCTCTCCAGCGAGCATGGCCACACATCTCGCGCGGAGCC 2535

QY 258 LysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGlu 277
DB 2536 AAGGATCTCGTCAAGNAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGCGTTCAG 2595

QY 278 AlaLeuCys- 280
DB 2596 GTCCTCAG-TAAGTACCCAGATCGTTGCTGTCATACATCATATGAATTGTATCGTTTCA 2654

QY 281 -----HisProTrpIleValAspGluGln 288
DB 2655 GAGCAACGATCGAGCGGATTTGGTGAACCTTGTAGATCACCCTGGATCAAGAGAGCGGA 2714

QY 289 AlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGlnPheSerGln 308
DB 2715 GACGCGCCTGACACGCGCTTGCACACGTTGTTCTCGACAGGCTCAAGCAGTTTCAGGGCC 2774

QY 309 MetAsnLysIleLysLysMetAlaLeuArgVal- 319
DB 2775 ATGAACCACTTCAAGAAACAGCATTTGAGGTACATTATCTGTATAAAGCTCCACAAATA 2834

QY 319 ----- 319

DB 2835 CAACCTTCTCAAGAACAGCAATGCTTACACGGCAGAAATTTTCATTATAAATGCTCTTGA 2894

QY 320 -----IleAlaGluArgLeuSerGluGluIleGlyGlyLeuLysGlu 334
DB 2895 ACATAATGTTAGATCATAGCTGGTGCCTTATCCGAAGAGGAGATCAACGGCTGAAGGAG 2954

QY 335 LeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAla 354
DB 2955 ATGTTCAAGAACATTGACAAAGATTAACACGCGGACCATTTACCTCGACGAGCTCAAAAC 3014

QY 355 GlyLeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAspAla 374
DB 3015 GGTGGTGCACAGCAGCGGCCCAAGCTGTTCAGACAGCAAAATGGAGAACTAATGGAAGCA 3074

QY 374 ----- 374

DB 3075 GTGAGTTTTTCAGAGTACAATCTTAAAAAAGGAATTTGTGATTTCTTTTCAAAATGAAGA 3134

QY 375 -----AlaAspIleAspAsnSe 380
DB 3135 TAATCTGAAAAACATCCTCCTGCTGAAATGCTTTATACATTTCCAGGCTGACGCTGACGGCAA 3194

QY 380 rGlyThrIleAspTyrGlyGluPheLeuAlaIleThrLeuHisMetAsnLysMetGluAr 400
DB 3195 CGGTTAATTTGACTACGACGAATTCGTACCCGCAACAGTGCATATCAACAACTGGATAG 3254

QY 400 gGluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGly- 417
DB 3255 AGAAGAGCACCTTTTACACAGCATTTCCAGTATTTTCGACAGGACAACAGCGG-GTAAGTTG 3313

QY 417 ----- 417

DB 3314 AACGTTAAATGATACAGCTGCTGTAATTTCTGGACAAACATATCATATAACAGACAC 3373

QY 418 -----TyrIleThrIleAspGluLeuGlnSerAlaCysTh 429
DB 3374 ATATATAATTCGTTTATCTCAGAGGTACATTACTAAAGAGAGCTTTGAGCAGCCTTGAA 3433

QY 429 rGluPheGlyLeuCysAspThr- - - - -ProLeuAspAspMetIleLysGluIleAspLeuAs 448
DB 3434 GAGCAAGGGTTGTATGACGCGCATAAATCAAAAGACATCATCTCCGATCGCCACTCTGA 3493

QY 448 phen- 449
DB 3494 CAA-TGTAAGGAACAACATTTATTTAAATTTTCAGCGCAAACTAACTATAGAAACCAC 3552

QY 449 ----- 449

DB 3553 ATCATGATATCAAAATTTTGAGGTGGCGGTGCTACAGAAATAGAACCCAGTACACCAAAAT 3612

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DB 3613 GACTAACTTGCATGATTAGTTTCTCCTCGTAACATGAACATTTGTGTTCTTAGTTCTTA 3672

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DB 3673 TTGTTAAACCAAGACTTAAATTCATCTTTTGCACATGCGAGGTGAAGATAGATTATTC 3732

QY 456 rGluPheThrAlaMetMetArgLysGly 465

QY 106 ValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArg 125
Db 1997 CTGTGGCGCGCGGAGCTCTTCGACCGCATCATCGCCGGCGCCAGTACACGGAGCGC 2056
QY 126 GluAlaValLysLeuLeuLeuThrLeuGlyValValGluAlaCysHisSerLeuGly 145
Db 2057 GGGCGCGCGGAGCTGTGCGCGCATCGTCGACATCGTCACACCTGCCACTCCATGGG 2116
QY 146 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAla 165
Db 2117 GTGATGACCGGACATCAAGCCCGAGAACTTCTGCTGCTCAAGAGGAGGAGCGG 2176
QY 166 LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr 185
Db 2177 CCGCTCAAGCCACCGACTTCGGCTCTCGCTCTTCTCAAGGAGGCGAGCTCCTCAGG 2236
QY 186 AspValValGlySerProTyrTyrValAlaProGluValLeuLysCysTyrGlyPro 205
Db 2237 GACATCGTCGCGAGCGCTACTATCATCGCGCGAGGTGCTCAAGAGAAAGTACGGCCG 2296
QY 206 GluLeuAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValProPro 225
Db 2297 GAGCGGACATCTGGAGCGTGGCGTCTGCTCTACATCTCTCGCGCGGCTGCCCTCC 2356
QY 226 PheTrpAla 228
Db 2357 TTCTGGGC-AGGTGGATCGTCCGTGTTCTGCTCTAGACGATATACAGAACCCGACGATG 2415
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Db 2416 GATTGCTTCTCAGCCCTGTTCTTTCATCACAGAGAACGAGACGTCATCTTCAACGCC 2475
QY 238 IleLeuGlnGlyLysLeuAspPheLysSerAspProTrpProThrIleSerGluAlaAla 257
Db 2476 ATCCTGGAGGAGCTTGACCTCTCCAGCGAGCATGGCCACACATCTCTCGCGGAGCC 2535
QY 258 LysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGlu 277
Db 2536 AAGGATCTGTCAGAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGGGTTCCAG 2595
QY 278 AlaLeuCys 280
Db 2596 GTCTCTAG-TAAGTACCAGATGTTGCTGTCTATACACTCATATGAATTTGTATCGTTCT 2654
QY 281 -----HisProTrpIleValAspGluGln 288
Db 2655 GACCAACGATCGAGCGGATTTGGTGAACCTTGTAGATCACCCATCGATCAAGAGACGGA 2714
QY 289 AlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGlnPheSerGln 308
Db 2715 GACGCGCTGACACGCGCTTGACACGTTGTTCTCGACAGGCTCAAGCAGTTTCAGGCGC 2774
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Db 2895 ACATAATGTTAGATCATAGTGGTGCCTATCCGAAGAGGAGATCACAGGCTGAGAGG 2954
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QY 375 -----AlaAspIleAspAsnSe 380
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Db 3195 CGGGTTAAATTGACTAGACGAATTCGTCCACCGCAACAGTGCATATGAACAAACTGGATAG 3254
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Db 3255 AGAAGAGCACCTTTACACAGCATTCCTCAGTATTTCGACCAAGGACAAACAGCGG-GTAAAGTTG 3313
QY 417 ----- 417
Db 3314 AACGTTAAATGATACAGCTGGTGTACCTGAAATTCCTGGACAAACACATATCATAAACAGGACAC 3373
QY 418 -----TyrIleThrIleAspGluLeuGlnSerAlaCysTh 429
Db 3374 ATATATAATTGCTTTTATCTCACAGGTACATTACTAAAGAAAGCTTGAGCACGCTTTGAA 3433
QY 429 rGluPheGlyLeuCysAspThr---ProLeuAspAspMetIleLysGluIleAspLeuAs 448
Db 3434 GGAGCAAGGTTGTATGACGCCGATAAATCAAAAGACATCTCTCCGATCCGACTCTGA 3493
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QY 450 -----AspGlyLysIleAspPheSe 456
Db 3673 TTGTTAAACCAAAAGACTTAAATTCACCTTTTTCACATGTCAGGATGGAAGGATAGATTATTC 3732
QY 456 rGluPheThrAlaMetMetArgLysGly 465
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RESULT 9

US-08-459-504B-26

; Sequence 26, Application US/08459504B

; Patent No. 6075185

GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; APPLICANT: Desai, Nalini M.

; APPLICANT: Lewis, Kelly S.

; APPLICANT: Kramer, Vance C.

; APPLICANT: Warren, Gregory W.

; APPLICANT: Evola, Stephen V.

; APPLICANT: Crossland, Lyle D.

; APPLICANT: Wright, Martha S.

; APPLICANT: Merlin, Ellis J.

; APPLICANT: Launis, Karen L.

; APPLICANT: Rothstein, Steven J.

; APPLICANT: Bowman, Cindy G.

; APPLICANT: Dawson, John L.

; APPLICANT: Dunder, Erik M.

; APPLICANT: Pace, Gary M.

; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COM:UTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CCG1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
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NAME/KEY: exon
LOCATION: 2691..2804
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NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:

NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
US-08-459-504B-26
Alignment Scores:
Pred. No.: 2,31e-118 Length: 4162
Score: 1159.50 Matches: 276
Percent Similarity: 50.00% Conservatives: 69
Best Local Similarity: 40.00% Mismatches: 115
Query Match: 44.72% Indels: 235
DB: 3 Gaps: 7
US-09-848-806-1 (1-495) x US-08-459-504B-26 (1-4162)
Qy 6 AsnProArgArgProSerAsnThrValLeuProTyrGlnThrProAtgLeuArgAspHis 25
Db 1698 AACCGCGCGCGCGGTG-GGCACGGTGTCTGGCGCGCCCATGGAGGACGTGCGCGCACC 1756
Qy 26 TyrLeuLeuGlyLysLysLeuGlyGlnGlyThrPheGlyThrTyrLeuCysThrGlu 45
Db 1757 TACTCGATGGGCAAGAGCTCGGCGCGGGCAGTTCGGCGGTGACGACCTGTGCGACGCAC 1816
Qy 46 LysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArg 65
Db 1817 CGGACGAGCGCGAGAGCTGGCTGCAAGACGATCGGAAGCGGAAGCTGGCGCCACGG 1876
Qy 66 GluAspTyrGluAspValTrpArgGluIleGlnIleMetHisHisLeuSerGluHisPro 85
Db 1877 GAGGACGTGACGACGTGCGCGCGGAGTGCAGATCATGCACCACTCTCCGCGCCAGCC 1936
Qy 86 AsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleValMetGlu 105
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Qy 106 ValCysGluGlyGlyLeuPheAspArgIleValSerLysGlyHisPheSerGluArg 125
Db 1997 CTGTGCGCGCGCGGAGCTCTTCACGCGCATCATCGCCGGGCGCCAGTACCGAGCGC 2056
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Db 2057 GCGCGCGCGAGCTGCTGCGCGCATCGTCAGATCGTCACACCTGCCACTCCATCGGG 2116
Qy 146 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAla 165
Db 2117 GTGATGCACCGGACATCAAGCGCGAGAACTTCTGTCTCAGCAAGGACGAGGACGCG 2176
Qy 166 LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr 185
Db 2177 CCGCTCAAGGCGCACCGACTTCGGCCCTCTCGTCTTCTTCAAGGAGGCGGAGCTCTCAGG 2236
Qy 186 AspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyrGlyPro 205
Db 2237 GACATCGTCGCGAGCGCTACTACATCGCGCGGAGGTGTCAAGAGAGAGTACGCGCGC 2296
Qy 206 GluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuSerGlyValPro 225
Db 2297 GAGCGGACATCTGGAGCGTTCGCGGTCTACATCTTCTTCGCGCGGCGTCCCTCC 2356
Qy 226 PheTrpAla----- 228
Db 2357 TTCTGGGC-AGGTGGATCGTCGTTGTCCTTAGACGATATACAGAACCCGACCATG 2415
Qy 229 -----GluThrGluSerGlyIlePheArgGln 237
Db 2416 GATTTCCTTCTAGCCCTGTTCCTTGCATCACCAGAGAACGAGACGCACTTTCACGCC 2475
Qy 238 IleLeuGlnGlyLysLeuAspPheLysSerAspProTrpProThrIleSerGluAlaA 257

2476 ATCTCGAGGGAGCTTGACCTCTCCAGCGAGCCATGGCCACACATCTCGCGGAGCC 2535
258 LysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgLysSerAlaHisGlu 277
2536 AAGGATCTGCTCAAGAGATGCTCAACATCAACCCCAAGGAGCGCTCACGGGTCCAG 2595
278 AlaLeuCys----- 280
2596 GTCTCTCAG-TAAGTACCAGATCGTTGCTGTCTATACACTCATATGAATTGTATGTTTCAT 2654
281 -----HisProTrrPileValaspGluIn 288
2655 GACCAACGATCGAGCGGATTTGGTGAACCTTGTAGATCACCCTGGATCAAGAAGACGGA 2714
289 AlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGlnPheSerGln 308
2715 GACGCGCTGACACGCGCTTGACAACTGTTCTCGACAGGCTCAAGCAGTTTCAGGGCC 2774
309 MetAsnLysIleLysLysMetAlaLeuArgVal----- 319
2775 ATGAACCAAGTCAAGAAAGCAGCATTTGAGGGTACATTATCTGATAAAAGCTCCACAAATA 2834
319 ----- 319
2835 CAACCTCTCGAAGAACAGCAATGCTTACAGCGCAGAAATTTTCATATAAATGCTCTTTGATG 2894
320 -----IleAlaGluArgLeuSerGluGluIleGlyGlyLeuLysGlu 334
2895 ACATAATGTTAGATCATAGCTGGTGCCTATCCGAGAGAGAGATCAACGGCTGAAGGAG 2954
335 LeuPheLysMetIleAspThrAspAsnSerGlyThrIlePheGluLeuLysAla 354
2955 ATGTTTCAAGAACTTACAGAGGATAACAGCGGACCATTTACCTCGACGAGCTCAAAAC 3014
355 GlyLeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetaspAla 374
3015 GGGTGGCAAGACAGCGGCCCAAGCTGTCCAGACAGCGAAATGGAGAACTAATGGAGCA 3074
374 ----- 374
3075 GTGAGTTTTTCAGAGTACAATCTTAAAAAAGGAATGTGATCTTTTCAAAATGAAGAAG 3134
375 -----AlaAspIleAspAsnSe 380
3135 TAAATCTGAAAAATCCTCTGCTGAAATGCTTTATACATTTCCAGGCTGACGCTGACGGCAA 3194
380 rGlyThrIleAspTyrGlyPheLeuAlaAlaThrLeuHisMetAsnLysMetGluAr 400
3195 CGGGTTAATGACTAGCAGCAATTCGTACCGCAACAGTGCATATGAACAAACTGGATAG 3254
400 gGluGluLeuValAlaAlaPheSerAspPheAspLysAspGlySerGly----- 417
3255 AGAAGAGCACCTTTACACAGCATTTCCAGTATTTCCAGACAGGACACAGCGG-GTAAGTTG 3313
417 ----- 417
3314 AACGTTAAATGATACAGCTGCTGTAATTTCTGGCAACACATATCATACAGGACAC 3373
418 -----TyrIleThrIleAspGluLeuGlnSerAlaCysTh 429
3374 ATATATAATTCGTTTATCTCAGGTACTACTAAAGAAGAGCTTGACGCGCTTGA 3433
429 rGluPheGlyLeuCysAspThr---ProLeuAspAspMetIleLysGluIleAspLeuAs 448
3434 GGAGCAGGGTTGTATGACGCGGATAAAATCAAGACATCATCTCCGATCGGACTCTGA 3493
448 pAsn----- 449
3494 CAA-TGTAAGGAACAAACATTATTTAAATTTTCAGCCGCAAACTAAACTATAGAAACCAC 3552
449 ----- 449

3553 ATCATGATCAAAATTTGAGGTGGCGTGTACAGAAATAGAACCCAGTACACCAAAAT 3612
449 ----- 449
3613 GACTAACTTGTCTCATGATTAGTTGTTCTCTCGTAACTGAACATTTGTGTCTTCTTCTTA 3672
450 -----AspGlyLysIleAspPheSe 456
3673 TTGTTAAACCAAGACTTAAATTCACATTTTGGCACATGCAGGATGGAAGGATAGATTATTC 3732
456 rGluPheThrAlaMetMetArgLysGly 465
3733 AGAGTTTGTGGCGATGATGAGGAAAGGG 3760

RESULT 10

US-08-459-444-26
Sequence 26, Application US/08459444A
Patent No. 6121014

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Launis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED

NUCLEIC ACID CODING SEQUENCE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,444A

FILING DATE: 02-Jun-1995

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 4162 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: misc feature

LOCATION: 1418..1427

OTHER INFORMATION: /note= "start of mRNA"

FEATURE:


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QY 375 -----AlaAspIleAspAense 380
Db 3135 TAATCTGAAACATCCCTGCTGAAATGCTTTATACATTTCCAGGCTGACGCTACGCGCA 3194
QY 380 rGlyThrIleAspTyxGlyPheLeuAlaIleThrLeuHisMetAsnLysMetGluAr 400
Db 3195 CCGGTTAATTCATGACGAAATTCGTCACCGCAACAGTCATATGAACAACTGGATAG 3254
QY 400 gGluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGly----- 417
Db 3255 AGAAGAGCACCTTTACACAGCATTCAGTATTTTCGACAGGACACACAGCGG-GTAAGTTG 3313
QY 417 ----- 417
Db 3314 AACGTTAAATGATACAGCTGGTACCTGAATTTCTGGACACACATATCATACAGGACAC 3373
QY 418 -----TyrlleThrIleAspGluLeuGlnSerAlaCysTh 429
Db 3374 ATATATAATTCGTTTATCTCACAGGTACATTAAGAGAGAGCTTGAGCACGCCCTTGAA 3433
QY 429 rGluPheGlyLeuCysAspThr---ProLeuAspAspMetIleLysGluIleAspLeuAs 448
Db 3434 GGAGCAAGGTTGTTATGACGCCGATAAATCAAAAGACATCATCTCCGATCCGACTCTGA 3493
QY 448 pAsn----- 449
Db 3494 CAA-TGTAAGGAACAAACATTATTTAAATTTACGCCGACAAACTAAACTATAGAAACCAC 3552
QY 449 ----- 449
Db 3553 ATCATGATACAAATTTTGAGGTGGCGGTGCTACAGAAATAGAACCCAGTACACCAAAT 3612
QY 449 ----- 449
Db 3613 GACTAACTTGTATGATTAGTTGTTCTCGTAACGAACTTTGTTCTTAGTTTCTTA 3672
QY 450 -----AspGlyLysIleAspPheSe 456
Db 3673 TTGTTAAACCAAGACTTAAATTCATCTTTTGCACATGCAGGATGGAAGATAGATTATTC 3732
QY 456 rGluPheThrAlaMetMetArgLysGly 465
Db 3733 ACAGTTTGTGGCATGATGAGGAAGGG 3760

RESULT 11
US-09-547-422-26
; Sequence 26, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: 1418..1427
; OTHER INFORMATION: /note= "start of mRNA"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1481..2366
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2367..2451
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2452..2602
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2603..2690
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2691..2804
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2805..2906
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2907..3075
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3076..3177
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3178..3304
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3305..3398
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3399..3498
; FEATURE:
; NAME/KEY: intron
; LOCATION: 3499..3713
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3714..3811
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-547-422-26
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Alignment Scores:

Pred. No.: 2,31e-118 Length: 4162
 Score: 1159.50 Matches: 276
 Percent Similarity: 50.00% Conservative: 69
 Best Local Similarity: 40.00% Mismatches: 115
 Query Match: 44.72% Indels: 235
 DB: 4 Gaps: 7

US-09-848-806-1 (1-495) x US-09-547-422-26 (1-4162)

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 DB 1698 AACCGCGCGCGCGT-GGCACGGTCTGGCGCGCCATCGAGGACGTGCGCGCAC 1756
 QY 26 TyrLeuLeuGlyLysLeuGlyGlnGlyPheGlyThrTyrLeuCysThrGlu 45
 DB 1757 TACTCGATGGCAAGGAGCTGGCGCGCGGACGTTCCGCGTGACGACCTGTGCACGCAC 1816
 QY 46 LysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArg 65
 DB 1817 CGGACGCGCGCGAGAGCTGGCGTCAAGACCATCGCAAGCGGAAGCTGGCGCGCACG 1876
 QY 66 GluAspTyrGluAspValTrpArgGluIleGlnIleMetHisHisLeuSerGluHisPro 85
 DB 1877 GAGGACGTGCACGACGTGGCGCGGAGTGCAGATCATGCACCATCTCTCGGCGCACGCC 1936
 QY 86 AsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleValMetGlu 105
 DB 1937 AACGTGGTGGCTCTCGCGCGCGGTACGAGGCAAGCAGCGTGCACCATCTGTCTGGAG 1996
 QY 106 ValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisSerGluArg 125
 DB 1997 CTGTGCGCGCGCGGAGCTCTTCGACCGCATCATGCGCGCGCGCGCATACGAGCGC 2056
 QY 126 GluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGly 145
 DB 2057 GCGCGCGCGAGCTGCTCGCGCGCATCGTGCAGATCGTGCACCATCTGCCACTCCATGGG 2116
 QY 146 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAla 165
 DB 2117 GTGATCACCGGACATCAAGCCCGAGAACTTCTGCTGCTCAGCAAGGACGAGGACGCG 2176
 QY 166 LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr 185
 DB 2177 CGGCTCAAGGCCACCGACTTCGCGCTCTCGTCTTCTCAAGAGGCGGAGCTGCTCAGG 2236
 QY 186 AspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyrGlyPro 205
 DB 2237 GATCGTGGCGAGCGCCTACTACATCGCGCGCGAGGTGCTCAAGAGGAAGTACGCGCGC 2296
 QY 206 GluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValPro 225
 DB 2297 GAGCGCGCATCTGGAGCGTGGCGTCTGCTCTACATCTTCTCGCGCGGCGTCC 2356
 QY 226 PheTrpAla----- 228
 DB 2357 TTCTGGGC-AGGTGGATCGTTCGTTCTGCTTAGACGATATACAGAACCGCAGT 2415
 QY 229 -----GluThrGluSerGlyIlePheArgGln 237
 DB 2416 GATTGCTTCTCAGCGCTGTTCTTGTCATCACCAGAGACGAGAACGCGCATCTTCAACGCGC 2475
 QY 238 IleLeuGlnGlyLysLeuAspPheLysSerAspProTrpProThrIleSerGluAlaAla 257
 DB 2476 ATCTCGGAGGCGAGGTTGACCTCTCCAGCGGCGCATGCGCCACACATCTCGCGCGGAGCC 2535
 QY 258 LysAspLeuIleTyrLysMetLeuGluArgSerProLysLeuArgIleSerAlaHisGlu 277
 DB 2536 AAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGGCTCAGCGGTTCAG 2595
 QY 278 AlaLeuCys----- 280

DB 2596 GTCTCTCAG-TAAGTACCAGATCGTTGCTGTCTATACACTCATATGAATTGTATCGTTTCAT 2654
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 DB 2655 GAGCAACGATCGAGCGGATTTGGTGAACCTTGTAGATCACCCATGGATCAAGAAGACGCGA 2714
 QY 289 AlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGlnPheSerGln 308
 DB 2715 GACGCGCTGCACACGCGCTTGACAAAGCTTGTCTCGACAGGCTCAAGCAGTTTCAGGCGC 2774
 QY 309 MetAsnLysIleLysLysMetAlaLeuArgVal----- 319
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 QY 319 ----- 319
 DB 2835 CAACTTCTGAAGAACAGCAATGCTTACACGGCAGAAATTTTTCATTATAAATGCTCTTGATG 2894
 QY 320 -----IleAlaGluArgLeuSerGluGluGluIleGlyGlyLeuLysGlu 334
 DB 2895 ACATAATGTTAGATCATAGCTGGTGCCTATCCGAAGAGAGATCACAGGCTGAAGGAG 2954
 QY 335 LeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAla 354
 DB 2955 ATGTTCAAGAACATTCGCAAGGATAACAGCGGACCATTTACCTCGACGAGCTCAACAC 3014
 QY 355 GlyLeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAspAla 374
 DB 3015 GGGTTGGCAAGCAGCGGCCCAAGCTGTCCAGACAGCGAAATGGAGAACTAATGGAAGCA 3074
 QY 374 ----- 374
 DB 3075 GTGAGTTTTTCAGAGTACAATCTTAAAAAAGGAATTTGTGATTTCTTTTCAAAATGAAGAAG 3134
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 DB 3135 TAATCTGAACAACATCCTCTGTAATGCTTTATACATTTCCAGGCTGACGCTCAGCGCAA 3194
 QY 380 rGlyThrIleAspTyrGlyPheLeuAlaIleThrLeuHisMetAsnLysMetGluArg 400
 DB 3195 CGGGTTAATGTACTACGCGAATTCGTCCACCGCAACAGTGCATATCAACAACTGGATAG 3254
 QY 400 gGluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGly----- 417
 DB 3255 AGAAGAGCACCTTTTACAGCATTCAGTATTTCCGAAGGACAAACAGCGG-GTAAGTTG 3313
 QY 417 ----- 417
 DB 3314 AACGTTAAATGATACAGCTGCTGTAATTTCTGACAAACACATATCATACAGGACAC 3373
 QY 418 -----TyrIleThrIleAspGluLeuGlnSerAlaCys 429
 DB 3374 ATATATAATTCGTTTATCTTCAGAGGTACATTTACTAAAGAAGAGCTTGAGCAGCGCTTGA 3433
 QY 429 rGluPheGlyLeuCysAspThr---ProLeuAspMetIleLysGluIleAspLeuAs 448
 DB 3434 GGAGCAAGGTTGTATGACGCGCAATAAATCAAGACATCATCTCCGATCGCGACTCTGA 3493
 QY 448 phen----- 449
 DB 3494 CAA-TGTAAGGAACAAACATTTTAAATTTTCAGCGCAAACTAAACTATAGAAACCAC 3552
 QY 449 ----- 449
 DB 3553 ATCATGATACAAATTTTGGGTGGCGTGTACAGAAATAGAACCCAGTACACCAAAAT 3612
 QY 449 ----- 449
 DB 3613 GACTAACTTGTCATGATTAGTTGTTCTCGTAACTGAACATTTGTGTTCTTAGTTTCTTA 3672
 QY 450 -----AspGlyLysIleAspPheSe 456
 DB 3673 TTGTTAAACCAAGACTTAAATTCATTTTTCACATGCGAGGATGGAGGATAGATTATTC 3732

Qy 456 rGluPheThrAlaMetMetArgLysGly 465
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RESULT 12

US-07-951-715A-26
; Sequence 26, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Review #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4165 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1416..1425
; OTHER INFORMATION: /note= "start of mRNA"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1481..2366
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2367..2449

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Db 2115 GTGATGACCGGGACATCAACCGGAGAACTTCTGCTGCTCAGCAAGGACGAGCGG 2174
Qy 166 LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr 185
Db 2175 CCGCTCAAGGCCACCGACTTCGGGCTCTCCGCTCTTCTCAAGGAGGGGAGCTGCTCAGG 2234
Qy 186 AspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyrGlyPro 205
Db 2235 GACATCGTCGCGACGCGCTACTACATCGCGCGCGAGGTGCTCAAGAGGAAGTACGGCGCG 2294
Qy 206 GluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValProPro 225
Db 2295 GAGCCGACATCTCGAGGTGCGGCTCATGCTCTACATCTTCTCCGCGGCGTGCCTCCC 2354
Qy 226 PheTrpAla----- 228
Db 2355 TTCTGGGC-AGGTCGGATCCGTCGCTGCTGTCTAGACGATATACAGAACCCGACGATG 2413
Qy 229 -----GluThrGluSerGlyIlePheArgGln 237
Db 2414 GATTGTGCTTCTACGCCCTGTTCTTTCATCACAGAGAACGAGACGGCATCTTCACGCGC 2473
Qy 238 IleLeuGlnGlyLysLeuAspPheLysSerAspProTrpProThrIleSerGluAlaAla 257
Db 2474 ATCTCGGAGGGAGCTTGACTCTCCAGCGGCGATGGCCACACATCTCCGCGGGAGCC 2533
Qy 258 LysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGlu 277
Db 2534 AAGGATCTCGTCAAGAAAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGGCGTTCAG 2593
Qy 278 AlaLeuCys----- 280
Db 2594 GTCCTCAG-TAAGTACCAGATCGTGTCTGTATACACTCATATGAATTTGTATGTTTCAT 2652
Qy 281 -----HisProTyrIleValAspGln 288
Db 2653 GAGCAACGATCGAGCGGATTTGGTGAACCTGTAGATCACCCTATGATCAAGAGACGGA 2712
Qy 289 AlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGlnPheSerGln 308
Db 2713 GACGCGCTGACAGCGCTTGACAACGTTGTTCTCGACAGGCTCAAGCAGTTCAGGCGC 2772
Qy 309 MetAsnLysIleLysMetAlaLeuArgVal----- 319
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Qy 319 ----- 319
Db 2833 CAACTTCTGAAGAACAGCAATGCTTACACGGCAGAAATTTTCATTATATAATGCTCTGATG 2892
Qy 320 -----IleAlaGluArgLeuSerGluGluIleGlyLeuLysGlu 334
Db 2893 ACATAATGTTAGATCATAGCTGGTGGCTATCCGAGAGGAGATCACAGGCTGAAGGAG 2952
Qy 335 LeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAla 354
Db 2953 ATGTTCAAGAACATTGCAAGGATAACAGCGGACCATTTACCTTCGACGAGCTCAACAC 3012
Qy 355 GlyLeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAspAla 374
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Db 3073 GTGAGTTTTCAGAGTACAATCTTAAAAAAGGAATTGTGATCTCTTTTCAAAATGAAGAAG 3132
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Db 3133 TAATCTGAAACATCCCTGCTGAATGCTTTATACATTTCCAGGCTGACGCTCAGCGGCAA 3192
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Db 3193 CCGGTTAATTGACTACGACGAATTCGTCACCGCAACAGTGCATATGAACAACTGGATAG 3252
Qy 400 gGluGluIleLeuValAlaIlePheSerAspPheAspLysAspGlySerGly----- 417
Db 3253 AGAAGACACCTTTTACACAGCATTTCCAGTATTTTCGACAGGACACAGCGG-GTAAGTTG 3311
Qy 417 ----- 417
Db 3312 AACGTTAAATGATACAGCTGGTACCTGAAATTTCTGGACAACACATATCATAAACAGGACAC 3371
Qy 418 -----TyrIleThrIleAspGluLeuGlnSerAlaCysTh 429
Db 3372 ATATATAATTGCTTTATCTCACAGGTACATTTACTTAAAGAGAGCTTCAGCACGCTTGA 3431
Qy 429 rGluPheGlyLeuCysAspThr---ProLeuAspAspMetIleLysGluIleAspLeuAs 448
Db 3432 GGAGCAAGGGTGTGTATGACGCCGATATAAATCAAAAGACATCATCTCCGATGCCGACTCTGA 3491
Qy 448 pAsn----- 449
Db 3492 CAA-TGTAAGGAACAAACATTATTATAATTTTCAGCCGACAACTATAAATATAGAAACAC 3550
Qy 449 ----- 449
Db 3551 ATCATGATATCAAAATTTTGAGTGGCGGTGCTACAGAAATAGAACCCAGTACACAAAT 3610
Qy 449 ----- 449
Db 3611 GACTAACTTGTCTGATGATTGTTGTTCTCGTAACTGAACATTTGTGTTCTTAGTTCTTA 3670
Qy 450 -----AspGlyLysIleAspPheSe 456
Db 3671 TTGTTAAACCAAGACTTAAATTCATTTTGCATGTCAGGATGGAAGGATAGATTATTC 3730
Qy 456 rGluPheThrAlaMetMetArgLysGly 465
Db 3731 AGAGTTTGTGGCGATGATGAGGAAGGG 3758

RESULT 13
US-09-347-801-3
; Sequence 3, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; EARLIER FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 2374
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-347-801-3

Alignment Scores:
Pred. No.: 3,03e-82 Length: 2374
Score: 831.00 Matches: 187
Percent Similarity: 58.30% Conservative: 94
Best Local Similarity: 38.80% Mismatches: 165
Query Match: 32.05% Indels: 36
DB: Gaps: 12

US-09-848-806-1 (1-495) x US-09-347-801-3 (1-2374)
Qy 26 TyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThrTyrLeuCysThrGlu 45
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QY 46 LysSerThrSerAlaAsnTyr-----AlaCysLysSerIleProLysArg 60
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QY 61 LysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMetHisHis 80
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QY 120 GlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGlu 139
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QY 280 CysHisProTrpIleValAspGluGlnAlaProAspLysProLeuAspProAlaVal 299
Db 1482 ACTCATCTCTGTTGTCGAGATGAACAAAGG-----CAGATCCCGCTGGACATACATC 1535
QY 300 LeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysMetAlaLeuArgVal 319
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QY 415 GlySerGlyTyrIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCys 434
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QY 435 AspThrPro-----LeuAspAspMetIleLysGluIleAspLeuAspAsnAspGly 451
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QY 452 LysIleAspPheSerGluPheThrAlaMetMet-----462
Db 1992 AAGCTAAACTTTCTCGGGTTTACCAAAATTTTACATGGTGTCAATAAGGGGCTCAAA 2051
QY 463 ---ArgLysGlyAspGlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPheAsn 481
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QY 482 IleAla 483
Db 2112 GCCGCT 2117
RESULT 14
US-08-464-164-1
; Sequence 1, Application US/08464164
; Patent No. 5614195
; GENERAL INFORMATION:
; APPLICANT: Tomley, Fiona M.
; APPLICANT: Dunn, Paul P. J.
; APPLICANT: Bumstead, Janene M.
; APPLICANT: Vermeulen, Arno N.
; TITLE OF INVENTION: Coccidiosis poultry vaccine
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Akzo No. 5614195el Patent Department
; STREET: 1300 Piccard Drive, Suite 206
; CITY: Rockville
; STATE: Maryland
; COUNTRY: U.S.A.
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: June 2, 1995
; APPLICATION NUMBER: US/08/464,164
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Gormley, Mary E.
; REGISTRATION NUMBER: 34,409
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 258-5200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1400 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Eimeria maxima
; STRAIN: Houghton
; DEVELOPMENTAL STAGE: sporozoite
; IMMEDIATE SOURCE:
; LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
; CLONE: Em70-1

; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: C-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Eimeria maxima
 ; STRAIN: Houghton
 ; DEVELOPMENTAL STAGE: sporozoite
 ; IMMEDIATE SOURCE:
 ; LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
 ; CLONE: Em70-1
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1368
 ; US-08-338-057-1

Alignment Scores:
 Pred. No.: 5,45e-76 Length: 1400
 Score: 771.50 Matches: 165
 Percent Similarity: 57.81% Conservative: 94
 Best Local Similarity: 36.83% Mismatches: 162
 Query Match: 29.75% Indels: 27
 DB: 1 Gaps: 8

US-09-848-806-1 (1-495) x US-08-338-057-1 (1-1400)

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 QY 58 ProLysArgLysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIle 77
 DB 79 TCTAAACGTCAGTAAACAGAGACAGATATAAGAAATTTATTATAAAGAGTTGAATTA 138
 QY 78 MetHisHisLeuSerGluHisProAsnValAlaTrgIleLysGlyThrTyrGluAspSer 97
 DB 139 TTAAGAAATTA---GATCATCTTAATATCATGAATTTATGAAATCTTTGAGGATAAA 195
 QY 98 ValPheValHisIleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleVal 117
 DB 196 GGATACTTTTATCTGTTACAGAAGTATATACAGGAGGAGAAATTAATTCATGAAATATT 255
 QY 118 SerLysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyVal 137
 DB 256 AATCGAAAAAGAAATTCAGCGAGCGGATCGTAGTACGTCTGATAGTACGTCAGGTCTATCGGCT 315
 QY 138 ValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeu 157
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Search completed: November 28, 2003, 13:22:43
 Job time : 138 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 28, 2003, 12:32:03 ; Search time 1177 Seconds

(without alignments)
1385.617 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

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Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2593	100.0	1747	12	US-10-289-172-2 Sequence 2, Appli

2	2593	100.0	1747	12	US-09-848-806-2	Sequence 2, Appli
3	2577	99.4	1488	10	US-09-938-842A-704	Sequence 704, App
4	2458	94.8	1657	12	US-10-289-172-4	Sequence 4, Appli
5	2458	94.8	1657	12	US-09-848-806-4	Sequence 4, Appli
6	1844.5	71.1	1473	10	US-09-938-842A-786	Sequence 786, App
7	1731	66.5	1635	10	US-09-938-842A-2344	Sequence 2344, Ap
8	1724	66.8	1635	10	US-09-938-842A-2334	Sequence 2334, Ap
9	1509.5	58.2	2230	9	US-09-828-313-26	Sequence 26, Appl
10	1381	53.3	1638	10	US-09-938-842A-1859	Sequence 1859, Ap
11	1313.5	50.7	1602	10	US-09-938-842A-2304	Sequence 2304, Ap
12	1277.5	49.3	1349	11	US-09-988-462-20	Sequence 20, Appl
13	1159.5	44.7	4162	11	US-09-988-462-26	Sequence 26, Appl
14	857.5	33.1	1387	9	US-09-828-313-13	Sequence 13, Appl
15	849	32.7	2253	9	US-09-828-313-25	Sequence 25, Appl
16	831	32.0	2374	10	US-09-854-731-3	Sequence 3, Appli
17	803.5	31.0	1800	10	US-09-938-842A-1063	Sequence 1063, Ap
18	726	28.0	455	9	US-09-770-444-571	Sequence 571, App
19	687	26.5	955	9	US-09-770-445-326	Sequence 326, App
20	591	22.8	1500	12	US-10-354-358-87	Sequence 87, Appl
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23	587.5	22.7	1480	12	US-10-204-041-9	Sequence 9, Appli
24	581.5	22.4	5637	10	US-09-917-800A-1537	Sequence 1537, Ap
25	578.5	22.3	1740	12	US-10-320-351-13	Sequence 13, Appl
26	578.5	22.3	1740	12	US-10-320-351-14	Sequence 14, Appl
27	578	22.3	1458	12	US-09-735-138-5	Sequence 5, Appli
28	569.5	22.0	1825	12	US-10-116-275-321	Sequence 321, App
29	568.5	21.9	2218	12	US-09-820-790-1	Sequence 1, Appli
30	565	21.8	1551	9	US-09-925-299-210	Sequence 210, App
31	565	21.8	1551	11	US-09-925-299-210	Sequence 210, App
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33	564.5	21.8	1578	12	US-10-175-042-6	Sequence 6, Appli
34	561.5	21.7	1733	14	US-10-037-270-526	Sequence 526, App
35	558.5	21.5	1694	12	US-10-355-975-3	Sequence 3, Appli
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39	543	20.9	1383	11	US-09-935-464-2	Sequence 2, Appli
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41	543	20.9	1738	11	US-09-935-464-4	Sequence 4, Appli
42	543	20.9	1738	14	US-10-125-835-4	Sequence 4, Appli
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44	538.5	20.8	981	12	US-10-090-002-1	Sequence 1, Appli
45	538.5	20.8	1372	10	US-09-817-181-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-10-289-172-2
; Sequence 2, Application US/10289172
; Publication No. US20030154504A1
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: Calcium Dependent Protein Kinase
; FILE REFERENCE: 00786/183002
; CURRENT APPLICATION NUMBER: US/10/289,172
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/201,925
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1747
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-289-172-2

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Pred. No.: 2593.00 Matches: 495
Score: 100.00%
Percent Similarity: 100.00%
Conservative: 0

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Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-848-806-1 (1-495) x US-10-289-172-2 (1-1747)

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QY 41 TyrLeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArg 60
DB 187 TATCTCTGCACAGAGAAATCAACCTCCGCTAAATTACGCCCTGCAATTCGATCCCGAAGCGA 246
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DB 727 AGCGGTGTTCTCCCTTCTGGGCAGAGACTGAGTCTGGAAATCTTTAGACAGATATTGCCA 786
QY 241 GlyLysLeuAspPheLysSerAspProTyrProThrIleSerGluAlaLysAspLeu 260
DB 787 GGGAAAGTTAGATTTCAAAATCTCACCGTGGCCCTACTATCTCAGAAGCTGCTAAAGATTG 846
QY 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCys 280
DB 847 ATCTATAAATGCTCGAAGGAGCCCCCAAGAACCGCATTTCTGCTCATGAAGCCCTGTGT 906
QY 281 HisProTyrIleValAspGluGlnAlaLalaProAspLysProLeuAspProAlaValLeu 300
DB 907 CACCCATGGATTGTCGATGAACAAGCAGCAGCAGACAGCCCTTGTATCCACAGCTCTTA 966
QY 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIle 320
DB 967 TCTCGCTAAAGCAGTTTCTCAAAATGAATAAGATTAAAGAAATGGCATTACCGGTAATT 1026
QY 321 AlaGluArgLeuSerGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAsp 340
DB 1027 GCTTGAGACTTTCAGAGGAAGAAATTTGAGGTCTGGAAGGAATTTGTTCAAGATGATAGAC 1086
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RESULT 2

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US-09-848-806-2
; Sequence 2, Application US/09848806
; Publication No. US20030167516A1
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: Calcium Dependent Protein Kinase
; TITLE OF INVENTION: Polypeptides as Regulators of Plant Disease Resistance
; FILE REFERENCE: 00786/389002
; CURRENT APPLICATION NUMBER: US/09/848,806
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/201,925
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1747
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-848-806-2
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Alignment Scores:
Pred. No.: 1,738-287 Length: 1747
Score: 2593.00 Matches: 495
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
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US-09-848-806-1 (1-495) x US-09-848-806-2 (1-1747)

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QY 1 MetGluThrLysProAsnProArgProSerAsnThrValLeuProTyrGlnThrPro 20
DB 67 ATGGAGACGAGCGCAAAACCTTAGACGCTCTTCAAAACACAGTTCTACCATATCAACACCA 126
QY 21 ArgLeuArgAspHisTyrLeuLeuGlyLysLysLeuGlyGlnGlyPheGlyThrThr 40
DB 127 CGATTAAAGAGATCATTTACCTTCTGGGAAAAAAGCTAGGCCCAAGGCCAATTTGGAACAACC 186
QY 41 TyrLeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArg 60
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Db 187 TATCTCGCAGAGAAATCAACTCCGCTAAATTACGCTGCAAAATCGATCCGGAAGCGA 246
Qy 61 LysLeuValCysArgGluAspTyrGluAspValTyrArgGluIleGlnIleMetHisHis 80
Db 247 AAGCTCGTGTGTCGCGAGAGATTACGAAGATGTATGCGGTGAGATTTCAGATCATGCATCAT 306
Qy 81 LeuSerGluHisProAsnValValAArgIleLysGlyThrTyrGluAspSerValPheVal 100
Db 307 CTCCTCTGAGCATCCAAATGTGTGTAGGATCAAAAGGGAATATGAAGATTTCGTTGTTGTT 366
Qy 101 HisIleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGly 120
Db 367 CATATTGTTATGAGGTTTGTGAAGGTGGTGAGCTTTTTCATCGGATGTGTTCTAAAGGT 426
Qy 121 HisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAla 140
Db 427 CATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAAAGCGATTCCTGGTGTGTGAGGCT 486
Qy 141 CysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSer 160
Db 487 TGTCAATCTCTTGGTGTATGATAGATAGATCTCAAACTGAGAAATTTCTTGTGTGATAGT 546
Qy 161 ProLysAspAlaLysLeuLysAlaThrAspPheGlyLysSerValPheTyrLysPro 180
Db 547 CCTAAAGATGATGCTAAGCTTAAAGCTTAAAGCTACCGATTTTGGTTGTCTCTCTATAAGCCA 606
Qy 181 GlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLys 200
Db 607 GCACAATATTTATAGCTAGTGTGAAGTCCGTACTATGTTGCACGAGGTGCTTAAG 666
Qy 201 LysCysTyrGlyProGluIleAspValTyrSerAlaGlyValIleLeuTyrIleLeuLeu 220
Db 667 AAATGTTATTGGACCTGAATAAGATAGTGTGGAGTGTGGTGTATCTCTACATTTTACTC 726
Qy 221 SerGlyValProPheThrPalaGluThrGluSerGlyIlePheArgGlnIleLeuGln 240
Db 727 ACGGTGTTCTCCCTTCCTGGCAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAA 786
Qy 241 GlyLysLeuAspPheLysSerAspProTyrProThrIleSerGluAlaAlaLysAspLeu 260
Db 787 GGGAGTTAGATTCAAAATCTGACCGGTGCGCTACTATCTCAGAGCTCTAAAGATTGT 846
Qy 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCys 280
Db 847 ATCTATAAAATGCTCGAAAGGAGCCCAAGAAACGCAATTTCTGCTCATGAAGCTTGTGT 906
Qy 281 HisProTyrIleValAspGluGlnAlaProAspLysProLeuAspProAlaValLeu 300
Db 907 CACCATGGAATGTGATGAACAAGCAGCAGCAGCAAGCCCTCTTGATCCAGAGTCTTA 966
Qy 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIle 320
Db 967 TCTCGTCTAAAGCAGTTTTCTCAAAATGAATAAGATTAAAGAAATGGCATTACGGTAA 1026
Qy 321 AlaGluArgLeuSerGluGluIleGlyLysLeuLysGluLeuPheLysMetIleAsp 340
Db 1027 GCTGAGAGACTTTCAGAGGAAGAAATTTGGAGTCTGAAGGAAATTTGTTCAAGATGATAG 1086
Qy 341 ThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGly 360
Db 1087 ACAGACAACAGCGGAACGATTTACTTTTGAAGAGCTCAAGCGGGTTTGAAGAGAGTCGA 1146
Qy 361 SerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSer 380
Db 1147 TCTGAACCTGATGGAATCAGAAATCAAGTCTCTCATGGATGCGGCTGATATCGACAACAGT 1206
Qy 381 GlyThrIleAspTyrGlyPheLeuAlaThrLeuHisMetAsnLysMetGluArg 400
Db 1207 GGTACATAGACTACGGAGAATTTCTTAGCAGCAACTTACACATGAACAAGATGGAGAGA 1266
Qy 401 GluGluIleLeuValAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThr 420
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Db 1267 GAGGAGATTCTGCTGCTGCATTTTTCGACTTTTGACAAAGACGGAAGCGGTTATATCAC 1326
Qy 421 IleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAsp 440
Db 1327 ATCGATGAGCTTCAGTCAGCTTCGACAGAGTTTGGTCTATGTGATACACCTCTGGAGC 1386
Qy 441 MetIleLysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAla 460
Db 1387 ATGATCAAGGAGATTGATCTTGACAAATGACGGGAAGATCGATTTCTCGGAGTTTACAG 1446
Qy 461 MetMetArgLysGlyAspGlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPhe 480
Db 1447 ATGATGAGGAAGGAGATCGAGTTGGGAGAGCAGAACCATGATGAAGAATCTTGAAC 1506
Qy 481 AsnIleAlaAspAlaPheGlyValAspGlyGluLysSerAspAsp 495
Db 1507 AACATTGCTGATGCTTTTGGAGTTGATGTTGAAAAATCTGATGAC 1551

RESULT 3
US-09-938-842A-704
; Sequence 704, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR APPLICATION DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 704
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-704

Alignment Scores:
Pred. No.: 9,388-286 Length: 1488
Score: 2577.00 Matches: 493
Percent Similarity: 99.60% Conservative: 0
Best Local Similarity: 99.60% Mismatches: 2
Query Match: 99.38% Indels: 0
DB: 10 Gaps: 0

US-09-848-806-1 (1-495) x US-09-938-842A-704 (1-1488)

Qy 1 MetGluThrLysProAsnProArgArgProSerAsnThrValLeuProTyrGlnThrPro 20
Db 1 ATGGAGACGAGGCCAAACCTTAGAGCTCTCTCAACACACAGTTCTACCATATCAACACCA 60
Qy 21 ArgLeuArgAspHisTyrLeuLeuGlyLysLysLeuGlyGlnPheGlyThrThr 40
Db 61 CGATTAGAGATCATTTACTCTCTGGAAAAAAGCTAGGCCAAGGCCAATTTGGAAACACC 120
Qy 41 TyrLeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArg 60
Db 121 TATCTCTGCAGAGAAATCAACCTCCGCTAATTACGCTGCAAAATCGAATCCCGAAGCGA 180
Qy 61 LysLeuValCysArgGluAspTyrGluAspValTyrArgGluIleGlnIleMetHisHis 80
Db 181 AAGCTCGTGTGTCGCGAGGATTACGAAGATGTATGCGGTGAGATTTCAGATCATGCATCAT 240
Qy 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100
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Db 241 CTCTCTGAGCATCCAAATGTTGTTAGGATCAAGGGACTTATGAAGATTTCGGTGTGTT 300
Qy 101 HisIleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGly 120
Db 301 CATATTGTTATGGAGGTTGTGAAGGTCGTGAGCTTTTGTGATCGGATTGTTCTTAAAGGT 360
Qy 121 HisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAla 140
Db 361 CATTTTAGTCGCGTGAAGCTGTCAAGCTTATTAAGACGATTCCTTGGTGTGTTGAGGCT 420
Qy 141 CysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSer 160
Db 421 TGTCAATCTCTGTTGTTATGCATAGAGATCTCAAACTCGAGAATTTCTTGTGATAGT 480
Qy 161 ProLysAspAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysPro 180
Db 481 CCTAAAGATGATGCTAAAGCTTAAGGCTAACCGATTGTTGTTGTTCTCTTATAAGCCA 540
Qy 181 GlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLys 200
Db 541 GGACATATTTATGACGTAGTTGGAAGTCGGTACTATGTTGCCACGAGGTGCTAAG 600
Qy 201 LysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu 220
Db 601 AAATGTTATGACCTGAAATAGATGTTGGAGTGTGGTGTATCTCTACATTTTACTC 660
Qy 221 SerGlyValProProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGln 240
Db 661 AGCGGTGTTCTCCCTCTCGGGCAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCA 720
Qy 241 GlyLysLeuAspPheLysSerAspProTrpProThrIleSerGluAlaAlaLysAspLeu 260
Db 721 GGGAGTTAGATTTTCAAAATCTGACCCGTGGCTACTATCTCAGAAGCTGCTAAAGATTG 780
Qy 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCys 280
Db 781 ATCTATAAAATGCTCGAAAGAGAGCCCAAGAAACGCAATTTCTGCTCATGAAGCCTTGT 840
Qy 281 HisProTrpIleValAspGluAlaAlaProAspLysProLeuAspProAlaValLeu 300
Db 841 CACCCATGGATGTGCGATGAACAAGCAGCAGCACCAAGCCCTCTGTATCCAGCAGCTTA 900
Qy 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIle 320
Db 901 TCTCGTCTAAAGCAGTTTCTCAATGAATGAATTAAGAAATGGCAATACGGGTAAATT 960
Qy 321 AlaGluArgLeuSerGluGluGluIleGlyLeuLysGluLeuPheLysMetIleAsp 340
Db 961 GCTGAGAGACTTTCAGAGGAAGAAATTTGGAGGTCTGAAGGAATTTGTTCAAGATCATAG 1020
Qy 341 ThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGly 360
Db 1021 ACAGACAAACAGCGGACGATTTACTTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTCGGA 1080
Qy 361 SerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSer 380
Db 1081 TCTGAACCTGATGGAATCAGAAATCAAGTCTCTCATGATGCGGTGATATCGACAAACAGT 1140
Qy 381 GlyThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArg 400
Db 1141 GGTACATAGACTACGAGAGATTCCTAGCAGCAACCTTACACATGAACAAGATGGAGAGA 1200
Qy 401 GluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThr 420
Db 1201 GAGGAGAACTGGTGGCTGCATTTCTACTTTGACAAAGACGGAACGGGTATATCACC 1260
Qy 421 IleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAsp 440
Db 1261 ATCGATGAGCTTCAGTCAGCTTGACAGAGTTTGGTCTATGTGATACACCTCTGGACGAC 1320
Qy 441 MetIleLysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAla 460
Db 1321 ATGATCAAGGAGATTGATCTTGAACAATGACGGGAAGATCGATTTCTCGGAGTTTACAGCA 1380
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Qy 461 MetMetArgLysGlyAspGlyValGlyValArgSerArgThrMetMetLysAsnLeuAsnPhe 480
Db 1381 ATGATGAGGAAAGGAGATGGAGTTGGGAGAGACAGAACCATGATGAGAACTTGAAC TTC 1440
Qy 481 AsnIleAlaAspAlaPheGlyValAspGlyGlyLysSerAspAsp 495
Db 1441 AACATTGCTGATGCTTTTGGAGTTTGATGGTGAATAAATCTGATGAC 1485
RESULT 4
US-10-289-172-4
; Sequence 4, Application US/10289172
; Publication No. US20030154504A1
; GENERAL INFORMATION:
; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: Calcium Dependent Protein Kinase
; FILE REFERENCE: Polypeptides as Regulators of Plant Disease Resistance
; CURRENT APPLICATION NUMBER: US/10/289,172
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/201,925
; FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1657
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-289-172-4
Alignment Scores:
Pred. No.: 5,15e-272 Length: 1657
Score: 2458.00 Matches: 470
Percent Similarity: 96.57% Conservative: 9
Best Local Similarity: 94.76% Mismatches: 13
Query Match: 94.79% Indels: 4
Gaps: 12
US-09-848-806-1 (1-495) x US-10-289-172-4 (1-1657)
Qy 4 LysProAsnProArgArgProSerAsnThrValLeuProTyrGlnThrProArgLeuArg 23
Db 7 AAACCAACCTCTAGNAGACCCTCAACAGTGTTCTTCATACGAAACACCAAGATTAGA 66
Qy 24 AspHisTyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThrTyrLeuCys 43
Db 67 GATCAGTATCTCTCGGCAAAAGCTAGGCCAAGGCCAATTTGGACCAACCTATCTCTGT 126
Qy 44 ThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuVal 63
Db 127 ACAGAGAAATCATCATCAGCTAATTACGCTTGCAAAATCAATCCCAAAACGTTAAGCTT 186
Qy 64 CysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMetHisLeuSerGlu 83
Db 187 TGTGCTGAAAGCTACGAGAGATGTATGCGTGAGATTGAGATCATGATCATCTCTCTGAG 246
Qy 84 HisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleVal 103
Db 247 CATCTTAATGTTGTAGAAATCAAGGGTACTTATGAGACTCTGTTTTTGTTCACATTGTT 306
Qy 104 MetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSer 123
Db 307 ATGGAAGTTTGTGAAGGTGGTGGCTTTTGTATCGGATTTGTTCTAAAGGGTGTGTAGT 366
Qy 124 GluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSer 143
Db 367 GAACGTGAAGCTCTAAGTTGATTAGACTATTCTTGGTGTGTTGAGGCTTGTTCATCT 426
Qy 144 LeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAsp 163
Db 427 CTTGGTGTATGATAGAGATCTTAAAGCTCGAGAAATTTCTTTGTTGATAGTCCAGTGAT 486
Qy 164 AspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyr 183
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Qy	244	AspPheLysSerAspProThrIleSerGluAlaAlaLysAspLeuIleTyrLys	263
Db	727	GATTTTAAATCTGATCCGCTACTACTCTCAGAAGGTGCTAAAGATTTCGATTACAAA	786
Qy	264	MetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCysHisProTrp	283
Db	787	ATGCTCGATAGAGCCCAAGAACGTAATTTCTGCACATGAAGCAATTGTGTACCCCTTGG	846
Qy	284	IleValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeu	303
Db	847	ATTGTTGATGAACATGCTGCACCAGACAAGCCTCTCGACCCAGCAGTCTTCTCGCGACTT	906
Qy	304	LysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAlaGluArg	322
Db	907	AAGCAGATTCTCGCAAAATGAATAAATCAAGAAAATGGCTTTACGAGTAATCCGCGAGAGA	966
Qy	324	LeuSerGluGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAspThrAspAsn	343
Db	967	CTCTCGGAGGAAGAGATTGGTGGTCTGAAGGAATTTGTTCAAATGATAGATACAGACAAC	1026
Qy	344	SerGlyThrIleThrPheGluLeuLysAlaGlyLeuLysArgValGlySerGluLeu	363
Db	1027	AGTGGAAACAATCACCTTTGAAGAGCTTAAACGAGTCTAAAGAGAGTTGGATCTGAATTG	1086
Qy	364	MetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGlyThrIle	383
Db	1087	ATGGAATCAGAAATCAAGTCTCTTATGGATCGCGCGGATATAGACAACAGTGGGACAATA	1146
Qy	384	AspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArgGluGluIle	403
Db	1147	GACTACCGTGAATTTCTTAGCAGCGACATTACATATAACAAGATGGAGAGAGAAGAAC	1206
Qy	404	LeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThrIleAspGlu	423
Db	1207	TTGTGTGTGGCTTTTCATCTTTGATAAAGATGTTAGCGGTTTATATCACCATTGACGAG	1266
Qy	424	LeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAspMetIleLys	443
Db	1267	CTTCAACAAGGCTCGACAGAGTTTGGTCTCTGTGCACACTCTCTCTTGATGATCATGATCAA	1326
Qy	444	GluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAlaMetMetArg	463
Db	1327	GAGATTGATCTTTGATTAATGACGGGAAGATTGATTTCTCAGAGTTTACTGCTATGATGAAG	1386
Qy	464	LysGlyAspGlyValGlyArgSerArgThrMetLysAsnLeuAsnPheAsnIleAla	483
Db	1387	AAAGGAGATGGTGTGGGAGGAGCAGAACTATGAGGAACAACCTTGAACATTCAATATAGCT	1446
Qy	484	AspAlaPheGlyValAspGly-----GluLysSerAspAsp	495
Db	1447	GAAGCTTTGGAGTTGAGGACACAAGCAGCAGCTCTAAATCTGATGAT	1494

RESULT 6

US-09-938-842A-786
; Sequence 786, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379

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Db 829 CATCCGTGGATTGTGGATGATAAGGTTGCTCCAGATAAAACCTTTGGACTCGCGGTAGTG 898
QY 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIle 320
Db 889 TCCCGCTGAAGAAGTTCTCGCAATGAACAACTTAAAGAAGATGGCTTTACGAGTTATT 948
QY 321 AlaGluArgLeuSerGluGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAsp 340
Db 949 GCAGAGAGACTATCTCAGGAAGAAATCGGTGGTCTCAACAGAACTGTTCAAAATGATAGAC 1008
QY 341 ThrAspAsnSerGlyThrIleThrPheGluGluLeuLysIleLysLysGluValGly 360
Db 1009 ACAGATAAAAGTGGGACTATCAGCTTTGAAGAGTTAAAGATAGTAGTAGACACGTGTGGG 1068
QY 361 SerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSer 380
Db 1069 TCAGAGCTTATGAATCAGAGATCCAGAACTCTTGGCTGGGCTGATGTTGATGAGAGT 1128
QY 381 GlyThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArg 400
Db 1129 GGAACAATGACTATCGAGAGTTCTTAGCTGCAACAATCCACTTGAACAAGCTGGAGAGA 1188
QY 401 GluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThr 420
Db 1189 GAGGAGAATCTAGTAGCTGCATTCTCTTCTTTGATAAGGATCCAAAGTGTATACACT 1248
QY 421 IleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAsp 440
Db 1249 ATCGAAGAGCTTCAACAGGCATGGAAGGAGTTTGGTATATAACGATTCATATCTTGATGA 1308
QY 441 MetIleLysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAla 460
Db 1309 ATGATCAAAAGACATTGATCAAGATAATGATGGACAAATAGACTATCGAGAAATTTGGGCA 1368
QY 461 MetMetArgGlyAspGlyValGlyArgSer-----ArgThrMetMetLysAsn 477
Db 1369 ATGATGAGGAAGAAATGGCACTGGAGGAGGAGTTGGTCGGAGAACTATGAGGAACCTCT 1428
QY 478 LeuAsnPhe 480
Db 1429 CTCAACTTT 1437
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RESULT 7

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US-09-938-842A-2344
; Sequence 2344, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2344
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2344
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Alignment Scores:
Pred. No.: 1,65e-188 Length: 1635
Score: 1731.00 Matches: 328
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Percent Similarity: 81.88% Conservative: 65
Best Local Similarity: 68.33% Mismatches: 85
Query Match: 66.76% Indels: 2
DB: 10 Gaps: 2
US-09-848-806-1 (1-495) x US-09-938-842A-2344 (1-1635)
QY 6 AsnProArgArgProSerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHis 25
Db 193 AAGTTTGACAACTTCTTACTATGTTCTTGGTCAACAAGACTCTTAACATTCGTGATCTT 252
QY 26 TyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThrTyrLeuCysThrGlu 45
Db 253 TACACGCTGAGTCGTAAAGTAGGACAAGGACAATTCGGGACAACGATTATTGTTGTTACTGAT 312
QY 46 LysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArg 65
Db 313 ATTGCCACAGGTTGTCACCTATGCTTGTAAAGTCTATATCCAAGAGGAAATGATATCTAAA 372
QY 66 GluAspTyrGluAspValTrpArgGluIleGlnIleMetHisLysLeuSerGluHisPro 85
Db 373 GAAGATGTTGAGGATGTTAGGAGGAGATTCAGATTATGTCATCATTTAGCTGGTCACAAG 432
QY 86 AsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleValMetGlu 105
Db 433 AATATTGTTACTATTAAAGCAGCTTATGAGGATCCTTTGTTGTTGTTTCCACATTGATGAG 492
QY 106 ValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArg 125
Db 493 CTTTGTGCTGGTGGTGAGTTGTTGATAGGATTATTTCATAGAGGTCATTACACGAGAGG 552
QY 126 GluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGly 145
Db 553 AAAGCTGCTGAGTTGACCAAGATCATTTGCGGTGTTGTTGAGCGGTGTCATTCTCTTGGT 612
QY 146 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAspAla 165
Db 613 GTTATGCATAGAGATTAAAGCCTGAGAAATTTCTTGTGTTAATAAGGATGATGATTC 672
QY 166 LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr 185
Db 673 TCTCTTAAGGCCATTGATTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 732
QY 186 AspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyrGlyPro 205
Db 733 GATGTTGTTGGAAGTCCATCATGTTGCTCTCTGAGGTTCTTCTAAACATTTATGTTCCA 792
QY 206 GluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValProPro 225
Db 793 GAAAGCTGATGTGTGGACTGCTGGTGTATATCTATCTATCTTACTAAGTGGTCCCGCCT 852
QY 226 PheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeuAspPhe 245
Db 853 TTCTGGGAGAAACACACGCAAGGAATATTGTGATGCTGTGTTGAAGGATATATTGACTTT 912
QY 246 LysSerAspProTyrProThrIleSerGluAlaAlaLysAspLeuIleTyrLysMetLeu 265
Db 913 GATACAGACCCCGTGGCTGTCTATATCCGACAGTGTCTAAAGATCTGATCCGGAAGATGTTA 972
QY 266 GluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCysHisProTyrIleVal 285
Db 973 TGCTCTAGTCCTTCTGAACGTTTGACTGCTCATGAAGTCTTCGCTCATCCATGATCTGT 1032
QY 286 AspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGln 305
Db 1033 GAGAAATGGAGTTGCACCGGATAGACACTTGACCCCGCTGTTTGTCTCGTCTAAACAG 1092
QY 306 PheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAlaGluArgLeuSer 325
Db 1093 TTTTCTGCAATGAATAAAATTAAGGAAGATGGCTTTAAAGGATGATAGCTGAGAGCCTCTCA 1152
QY 326 GluGluGluIleGlyLeuLysGluLeuPheLysMetIleAspThrAspAsnSerGly 345
Db 1152 TTTTCTGCAATGAATAAAATTAAGGAAGATGGCTTTAAAGGATGATAGCTGAGAGCCTCTCA 1152
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QY 382 ThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArgGlu 401
Db 1516 ACAATAGATTACAAAGAGTTTCATAGCTGCAACATTACATCTAAACAATAAGAGAGAG 1575
QY 402 GluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyThrIleThrIle 421
Db 1576 GACCATTTGTTGCGAGCTTTTACATACCTTTGACAAAGATGGAGCGGCTATATCACCCCA 1635
QY 422 AspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAspMet 441
Db 1636 GACAGCTTCACACAGCTTGTGAGGATTTGGTGTGAGGATGTCGCCATAGAGAACTG 1695
QY 442 IleLysGluLeuAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAlaMet 461
Db 1696 ATCGCGCATGTTGATCAAGACAATGACGGCGGAATAGACTACAACGAGTTTGTGGCGATG 1755
QY 462 MetArgLysGlyAspGlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPheAsn 481
Db 1756 ATCGAGAAAGGAAGCATCACAGGAGGACCTGTGAAAAATGGTCTAGAGAAAAAGCTTTAGC 1815
QY 482 IleAla 483
Db 1816 ATTGCT 1821

RESULT 9

US-09-828-313-26
; Sequence 26, Application US/09828313
; Patent No. US20020059662A1
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: THIELEN, NOCHA VAN
; APPLICANT: CHEN, ROUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; TITLE OF INVENTION: USE IN PLANTS
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2230
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-313-26

Alignment Scores:
Pred. No.: 7,3e-163 Length: 2230
Score: 1509.50 Matches: 290
Percent Similarity: 75.47% Conservative: 70
Best Local Similarity: 60.80% Mismatches: 112
Query Match: 58.21% Indels: 5
DB: 9 Gaps: 3

US-09-848-806-1 (1-495) x US-09-828-313-26 (1-2230)

QY 5 ProAsnProArgArgProSerAsnThr-----valLeuProTyrGlnThrProArg 21
Db 531 CCGAGGCCGAAGCCAGCATCGAGGTACGTATCCGGTGTGTTGGGTAAAGCCGCTGTGCAGAT 590
QY 22 LeuArgAspHisTyrThrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThrTyr 41
Db 591 ATTGCTCAATCTTACATCTCGGACCGGAGCTTGGCCGAGGCGAGTTCGGAGTGACTTAC 650
QY 42 LeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLys 61
Db 651 TTGTGTACTGACAAGATGCAATGAGGCGGTACGGCTGCAAGAGCATGCCAAACCGAAA 710
QY 62 LeuValCysArgGluAspTyrGluAspValTyrArgGluIleGlnIleMetHisLeu 81
Db 711 CTGACCAGTAAGGAGGATATCGAGGATGTTAAGCGGAGGTTTCAGATTATGTCATCACCTG 770
QY 82 SerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheValHis 101
Db 771 TCGGGGACACCCCAATATCGTGGTGTAAAGGATGTGTTCGAGGACAAGCATTCCTCGTCAT 830
QY 102 IleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHis 121
Db 831 CTTGTGATGAGCTCTGTGCGAGGTGGCGACTCTTCGATCGCATCATTCGCAAGGGCAT 890
QY 122 PheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCys 141
Db 891 TACAGTGAGCGCGCCGCTGCGCATATCTGCGAGAGTCATCTCAATGTGGTGCACAGATGC 950
QY 142 HisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerPro 161
Db 951 CACTCATATTAGGGTCTTCATCGGGATCTCAAGCCAGAGAATTTCTGTGTGGCCAGCAAG 1010
QY 162 LysAspAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGly 181
Db 1011 GCTGAGATGCGCTCTGAAGGCCACAGACTTCGGTCTGTCAACTTTCTTTAAGCCAGGA 1070
QY 182 GlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLysLys 201
Db 1071 GATGTGTTCCAGGATATTGTGGAAGTGGGTATTACGTGCGCCCTGAAGTTTGAAGAGA 1130
QY 202 CysTyrGlyProGluIleAspValTyrSerAlaGlyValIleLeuTyrIleLeuLeuSer 221
Db 1131 AGTTATGGTCTCTGAAGCTGATGTTTGGAGTGCAGGCGTGTGTTGTATACATCTCTGT 1190
QY 222 GlyValProProPheThrAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGly 241
Db 1191 GGTGTACCCCTTCTGGGCTGAATCTGACGAGGATATCTTTGACGCTGTGCTCAAGGG 1250
QY 242 LysLeuAspPheLysSerAspProTyrProThrIleSerGluAlaLysAspLeuIle 261
Db 1251 CACATAGACTTCGAGAACGATCCATGCGCGAAATCTCCAACCGGGCTAAGGATTGGTG 1310
QY 262 TyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCysHis 281
Db 1311 AGGAAATGCTAAACCTTAACGTGAAGATACGCTCTGACGCGCACAGCGGTGTTGAACCAT 1370
QY 282 ProTyrIleValAspGluGlnAlaProAspLysProLeuAspProAlaValLeuSer 301
Db 1371 CATGATGAAGAGATGTTGATGCTCCAGAGTCCACTCGACATTCGGTGTGTTGACC 1430
QY 302 ArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAla 321
Db 1431 AGACTGAAAAATTTCTCAGCGCCCAACAAGATGAAAAAGCTGCGCTGAAGGTGATTGCA 1490
QY 322 GluArgLeuSerGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAspThr 341
Db 1491 GAGAGTCTGTCGAGGAGAGATCGTGGGTGAGGAGATGTTCAAAATCCATAGATACA 1550
QY 342 AspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGlySer 361
Db 1551 GACAACAGCGGCACCGTGACGTTCGAGGAGCTTAAGAAAGGGTTCGTGAAGCGGGCTCA 1610
QY 362 GluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGly 381
Db 1611 AAACTTAATGATCGACATCAGAAACTAATGGAAGCTGCGAGTGTCCATGGAAACGGC 1670
QY 382 ThrIleAspTyrGlyGluPheLeuAlaThrLeuHisMetAsnLysMetGluArgGlu 401
Db 1671 AAGATCGACTTCAACGAGTTTCATATCGGCAACAATGCAATGAAACAAGACGGAAGAG 1730
QY 402 GluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyThrIleThrIle 421
Db 1731 GATCACCTTTGGCGAGCATTCATGCTTTCGACGCAATAGCGGGTATATCACCATC 1790
QY 422 AspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAsp---ThrProLeuAspAsp 440
Db 440


```
RESULT 11
US-09-938-842A-2304
; Sequence 2304, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCDP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2304
; LENGTH: 1602
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2304

Alignment Scores:
Pred. No.: 1,47e-140 Length: 1602
Score: 1313.50 Matches: 248
Percent Similarity: 72.89% Conservative: 88
Best Local Similarity: 53.80% Mismatches: 118
Query Match: 50.66% Indels: 7
DB: 10 Gaps: 3

US-09-848-806-1 (1-495) x US-09-938-842A-2304 (1-1602)
QY 26 TyrLeuLeuGlyLysLysLeuGlyGlnGlnPheGlyThrThrTyrLeuCysThrGlu 45
Db 169 TATGATCTGGGCGTGAGGTGTGCGGGAGAGTTGGTATTACTTGTGCACTGAT 228
QY 46 LysSerThrAlaAsnTyrAlaCysLysSerIleProLysLysArgLysLeuValCysArg 65
Db 229 ATCAAAACGGCGCAGAGTATGCGTCAAGTCTATATCAAGAAGAGCTTGAACAGCT 288
QY 66 GluAspTyrGluAspValTrpArgGluIleGlnIleMethHisLeuSerGluHiePro 85
Db 289 GTGATATAGAGGATGTTAGGAGGGAAGTTGAGATAATGAACAATATGCTACACACCA 348
QY 86 AsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleValMetGlu 105
Db 349 AATATCGTGTGCTGAAGGATGCTTTGAGGATGATGATGATGATGATGATGATGATG 408
QY 106 ValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArg 125
Db 409 TTGCTGGAAGAGCTGAGCTGTTGATCGGATTTGCTAGAGTCTATTATATCTAGCCGA 468
QY 126 GluAlaValLysLeuLysThrIleLeuGlyValValGluAlaCysHisSerLeuGly 145
Db 469 GCTGCTGCTGCGATGATGAAGACTATTCTTGAAGTTGTTGAGATATGCCAATAGCATGGA 528
QY 146 ValMetHisArgAspLysProGluAsnPheLeuPheAspSerProLysAspAspAla 165
Db 529 GTGATCATCGGAGCTTAAGCCTGAGAACTTCTCTTTCGCAATATAAAGAGACATCA 588
QY 166 LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr 185
Db 589 GCCCTTAAGCCATAGATTTGGATTATCAGTCTCTTCAAGCCTGCTGAGGATCAAC 648
QY 186 AspValValGlySerProTyrTyrValAlaProGluValLysLysCysTyrGlyPro 205
Db 649 GAGATTGTTGGAAGTCTTATTACATGGCCAGAGGATCTTAGGGCAATATTACGGACCT 708
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QY 206 GluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValPro 225
Db 709 GAGTTGATATCTGGAGTGTGAGTTATCTTTATATCTGCTCTGCTGTTGCCACCA 768
QY 226 PheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeuAspPhe 245
Db 769 TTTTGGCCGAGACTGAGCAAGGGGTGGCTCAGCGCATCATTAGTTCAGTTATCGACTTT 828
QY 246 LysSerAspProTrpProThrIleSerGluAlaLysAspLeuIleTyrLysMetLeu 265
Db 829 AAGAGGATCCATGGCCGAGAGTTCTGAGCTGCCAAGACCTTTGAGAGAAAGTCTC 888
QY 266 GluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCysHisProTrpIleVal 285
Db 889 GAACCTGACCCCAAAAAACGGCTTCTGCTGCACAAGTACTCGAACATCTTGGATACAA 948
QY 286 AspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGln 305
Db 949 AATGCGAAGAGGCTCCAAATGTTTCACTCGGGGAGACGGTGAAGCAAGACTCAACACAG 1008
QY 306 PheSerGlnMetAsnLysIleLysMetAlaLeuArgValIleAlaGluArgLeuSer 325
Db 1009 TTTTCTGTTATGAACAGCTCAAGAAAGAGCCCTACGGGTGATAGCCGAACACTTATCA 1068
QY 326 GluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAspThrAspAsnSerGly 345
Db 1069 GTGAGGAGTAGCTGCGCATCAAGGAAGCATTTGAGATGATGACACATGAAGACCGGA 1128
QY 346 ThrIleThrPheGluLeuLysAlaGlyLeuLysArgValGly---SerGluLeuMet 364
Db 1129 AAGATAAACCTCGAGGAGCTTAAATTTGGACTTTCATAAACTCGGACAGCAGATACCT 1188
QY 365 GluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGlyThrIleAsp 384
Db 1189 GATACCTGATCTACAGATTCTGATGGAGGCTGCTGATGTTGATGGGATGGGACTTTAAAT 1248
QY 385 TyrGlyGluPheLeuAlaThrLeuHisMetAsnLysMetGluArgGluIleLeu 404
Db 1249 TATGGGAGTTTGTGCTGTCTGTGCTCTTTAAGAAATGCGAAGACGACACACTTG 1308
QY 405 ValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThrIleAspGluLeu 424
Db 1309 CATAAAGCTTTTGTGCTTTTGTGACCAAGATTCAGAGCGATTACATAGAGATTGAGGAGCTG 1368
QY 425 GlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAspMetIle---- 442
Db 1369 CGTGAGCTTTAAATGAT-----GAGGTGGATACTAACAGTGAAGAAGTTGTGACGT 1422
QY 443 -----LysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAla 460
Db 1423 ATTATGCAAGATGTTGACACAGACAGGACGGACGAATAAGCTTATGAAGAGTTTGGCGCG 1482
QY 461 MetMetArgLysGlyAspGlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPhe 480
Db 1483 ATGATGAAGCTGGAAACAGATTGGAGGAAGCGTCGAGGCGAGTATTTCCCGGGAAGATTC 1542
QY 481 Asn 481
Db 1543 AAC 1545

RESULT 12
US-09-988-462-20
; Sequence 20, Application US/09988462
; Publication No. US20030046726A1
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
```

Wright, Martha S.
Merlin, Ellis J.
Launie, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 09/988,462

FILING DATE: 20-No. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-188051

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

OTHER INFORMATION: /note= "cDNA sequence for maize

pollen-specific calcium dependent protein kinase gene as

disclosed in Figure 30."

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-09-988-462-20

Alignment Scores:

Pred. No.: 1

Score: 1277.50

Percent Similarity: 76.98%

Best Local Similarity: 61.89%

Query Match: 49.27%

DB: 11

Gaps: 1

Length: 1349

Matches: 242

Conservative: 59

Mismatches: 89

Indels: 1

Gaps: 1

US-09-848-806-1 (1-495) x US-09-988-462-20 (1-1349)

QY 76 GlnileMethHisLeuSerGluHisProAsnValValargLleLysGlyThrTy-Glu 95

Db 3 CAGATCATGACCACTCTCCGGCCAGCCCAACGTGGTGGCCCTCCCGCGCGGTACGAG 62

QY 96 AspSerValPheHisIleValMetGluValCysGluGlyGlyGluLeuPheAspArg 115

Db 63 GACAAGCAGAGCGTGCACCTCGTCATGAGCTGTGCGCGCGGGGAGCTCTTCGACCGC 122

RESULT 13

QY 116 IleValSerLysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeu 135
Db 123 ATCATCGCCCGGCGCAGTACACGAGCGCGCGGAGCTCTCGCGCCATCGTG 182
QY 136 GlyValValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsn 155
Db 183 CAGATCGTGACACCTGCCACTCCATGGGGTGATGACACCGGACATCAAGCCCGAGAAC 242
QY 156 PheLeuPheAspSerProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSer 175
Db 243 TTCCTGTCTCTCAGCAAGGACGAGCGCGCTCAAGGCGCACCGACTTCGCGCTCTCC 302
QY 176 ValPheTyLysProGlyGlnTyLysPheValValGlySerProTyLysValAla 195
Db 303 GTCTTCTCAAGGAGCGGAGCTCTCAGGACATCTCGCGAGCGCTACTACATCGCG 362
QY 196 ProGluValLeuLysLysCysTyLysProGluLysAspValTrpSerAlaGlyValIle 215
Db 363 CCCGAGGTGCTCAAGAGGAAGTACGCGCCGAGGCGGACATCTGGAGGCTCGCGTCATG 422
QY 216 LeuTyLysLeuSerGlyValProPheTrpAlaGluThrGluSerGlyIlePhe 235
Db 423 CTCTACATCTTCTCGCGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 482
QY 236 ArgGlnIleLeuGlnGlyLysLeuAspPheLysSerPheProTrpProThrIleSerGlu 255
Db 483 ACCGCCATCTCGCGAGGCGAGCTTACCTCTCCAGCGAGCATCGGCGCACACATCTCGCG 542
QY 256 AlaAlaLysAspLeuIleTyLysMetLeuGluArgSerProLysLysArgIleSerAla 275
Db 543 GGAGCCAAAGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGGAGCGGCTCAGCGG 602
QY 276 HisGluAlaLysCysHisProTrpIleValAspGlnAlaAlaProAspLysProLeu 295
Db 603 TTCAGGTCTCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 662
QY 296 AspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMet 315
Db 663 GACAACGTTGTTCTCGACAGCTCAAGCGTTCAGGCGCATGAACCATTTCAAGAAAGCA 722
QY 316 AlaLeuArgValIleAlaGluArgLeuSerGluGluIleGlyGlyLeuLysGluLeu 335
Db 723 GCATTGAGGATCATAGCTGGGTGCTATCCGAGAGGAGATCAAGGGCTCAGAGGATG 782
QY 336 PheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGly 355
Db 783 TTCAGAAACATTGACAGGATTAACAGCGGAGCATTTACCTCTCGACGAGCTCAAAACAC 842
QY 356 LeuLysArgValGlySerGluLeuMetGluSerGluLysSerLeuMetAspAlaAla 375
Db 843 TTGCAAAAGCAGCGGCCCAAGCTGTGACAGCGGAAATGGAGAACTTAATGGAAGCAGCT 902
QY 376 AspIleAspAsnSerGlyThrIleAspTyLysGlyGluPheLeuAlaAlaThrLeuHisMet 395
Db 903 GACGCTCAGCGCAACGGGTTAATTGACTACGAGCAATTCGTCACCGCAACAGTCATATG 962
QY 396 AsnLysMetGluArgGluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGly 415
Db 963 AACAACTGGATAGAGAAGAGCACCTTTACACAGCATTTCCAGTATTTTCGACAGGACAAC 1022
QY 416 SerGlyTyLysIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAsp 435
Db 1023 AGCGGTACTATTACTAAAGAGAGCTTGAAGCAGCGCTTGAAGGAGCAAGGGTCTGTATGAC 1082
QY 436 Thr---ProLeuAspMetIleLysGluIleAspLeuAspAsnAspGlyLysIleAsp 454
Db 1083 GCGGATAAAATCAAGAGACATCATCTCCGATGCGGAGCTCTGCAATGATGAGAGATAGAT 1142
QY 455 PheSerGluPheThrAlaMetMetArgLysGly 465
Db 1143 TATTGAGGTTTGTGCGGATGATGAGGAAAGGG 1175
RESULT 13

US-09-988-462-26
: Sequence 26, Application US/09988462
: Publication No. US20030046726A1
: GENERAL INFORMATION:
: APPLICANT: Kozziel, Michael G.
: Desai, Nalini M.
: Lewis, Kelly S.
: Kramer, Vance C.
: Warren, Gregory W.
: Evola, Stephen V.
: Crossland, Lyle D.
: Wright, Martha S.
: Merlin, Ellis J.
: Launis, Karen L.
: TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
: INSECTICIDAL ACTIVITY IN MAIZE
: NUMBER OF SEQUENCES: 94
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Syngenta Biotechnology, Inc.
: STREET: 3054 Cornwallis Road
: CITY: Research Triangle Park
: STATE: NC
: COUNTRY: USA
: ZIP: 27709
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/988,462
: FILING DATE: 20-No. US20030046726A1-2001
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 09/547,422
: FILING DATE: 11-APR-2000
: APPLICATION NUMBER: US 08/459,504
: FILING DATE: 02-JUN-1995
: APPLICATION NUMBER: US 07/951,715
: FILING DATE: 25-SEP-1992
: APPLICATION NUMBER: US 07/772,027
: FILING DATE: 04-OCT-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Meigs, J. Timothy
: REGISTRATION NUMBER: 38,241
: REFERENCE/DOCKET NUMBER: S-188051
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (919)541-8587
: TELEFAX: (919)541-8689
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4162 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHETICAL: NO
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: 1418..1427
: OTHER INFORMATION: /note= "start of mRNA"
: FEATURE:
: NAME/KEY: exon
: LOCATION: 1481..2366
: FEATURE:
: NAME/KEY: intron
: LOCATION: 2367..2451
: FEATURE:
: NAME/KEY: exon
: LOCATION: 2452..2602
: FEATURE:
: NAME/KEY: intron
: LOCATION: 2603..2690

FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-988-462-26
Alignment Scores:
Pred. No.: 2,96e-122 Length: 4162
Score: 1159.50 Matches: 276
Percent Similarity: 50.00% Conservative: 69
Best Local Similarity: 40.00% Mismatches: 115
Query Match: 44.72% Indels: 235
DB: 11 Gaps: 7
US-09-848-806-1 (1-495) x US-09-988-462-26 (1-4162)
QY 6 AsnProArgArgProSerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHis 25
Db 1698 AACCGCGCGCGCGGTG-GGCACGGTCTGGGCGGCCCATGGAGGACGTGGCGCGAC 1756
QY 26 TyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThrTyrLeuCysThrGlu 45
Db 1757 TACTCGATGGCAAGAGCTCGGCGCGCGGCGATTCTCGCGTGACGACCTGTGCACGCAC 1816
QY 46 LysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArg 65
Db 1817 CGGACGCGCGCGAGAGCTGGCTGCAAGACGATCGCGAGCGGAGCTGGCGCGCAGG 1876
QY 66 GluAspTyrGluAspValTrpArgGluIleGlnIleMetHisHisLeuSerGluHisPro 85
Db 1877 GAGGACGTGACGACGTGGCGCGGAGGTGCAGATCATGCACCCACCTCTCCGCGCCAGCCC 1936
QY 86 AsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleValMetGlu 105
Db 1937 AACGTGGTGGCTCTCGCGCGCGCTACGAGGCAAGACGAGCGTGCACCTCGTCATGGAG 1996
QY 106 ValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArg 125
Db 1997 CTGTGGCGCGCGGGGAGCTCTTCACCGCATCATCGCCCGGGCCAGTACACGGAGCGC 2056
QY 126 GluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGly 145
Db 2057 GCGCGCGCGGAGCTGTGGCGCCCATCTGTCACGCTGTCACACCTGCCCTCCATCGGG 2116
QY 146 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAspAla 165
Db 2117 GTGATGCACCGGGACATCAAGCCCGAGAACTTCTCTGCTGCTCAGCAAGACGAGGACGG 2176
QY 166 LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr 185


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Qy 218 IleLeuLeuSerGlyValProPheTirpAlaGluThrGluSerGlyIlePheArgGln 237
Db |||||
1050 ATTTTGTATGTGTAGTCGACCGTTTGGCGCGGACCGAGTCGGGCATTTTCGTGCG 1109
Qy 238 IleLeuGlnGlyLysLeuAspPheLysSerPheProTirpProThrIleSerGluAla 257
Db |||||
1110 GTGTTGAGGGGTGACCCGAGCTTTGAAGAAGCCCTTGGCCCTCCATCTCTCCGAAGCC 1169
Qy 258 LysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGlu 277
Db |||||
1170 AAGGATTCGTGAAGCGTCTCTGAATAGGATATGCCGAACCGCATGCTGTCACAA 1229
Qy 278 AlaLeuCysHisProTirpIleValAspGluGlnAlaAlaProAspLysProLeuAspPro 297
Db |||||
1230 GCTTTAACTCATCCATGATTCGAAGTAACAACGTG-----AAGATACCTCTGGATATC 1283
Qy 298 AlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeu 317
Db |||||
1284 TTAGTGTACAGACTGTGAGGAATTTATCTCGTCATCATCCATGAGAAAGGCTGCTTTG 1343
Qy 318 ArgValIleAlaGluArgLeuSerGluGluGlyGlyLeuLysGluLeuPheLys 337
Db |||||
1344 AAGGCCCTGTCAAGACTTTAACCGAAGACGAGACTTTTATCTACTGACTCAATTTATG 1403
Qy 338 MetIleAspThrAspAsnSerGlyThrIlePheGluGluLeuLysAlaGlyLeuLys 357
Db |||||
1404 CTGCTAGAACCAAGTAACACGGTGTACTTTTGAGAAATTTTCAGACAGGCACCTGCTG 1463
Qy 358 ArgValGlySerGluLeuMet--GluSerGluIleLysSerLeuMetAspAlaAlaAsp 376
Db |||||
1464 AAAAATTCACAGAGGCCATGAAAGAGTCACGGGTTTGTGAATTCGAAATCGATGGAT 1523
Qy 377 IleAspAsnSerGlyThrIleAspTyrGlyPheLeuAlaAlaThrLeuHisMetAsn 396
Db |||||
1524 GGTCTTCATTTCAAGAAATGCACTTTTCAGAGTTCTGTGCGCGGCCATTAGTGTCTC 1583
Qy 397 LysMetGluArg-----GluGluIleLeuValAlaAlaPheSerAspPheAsp 412
Db |||||
1584 CAGTTAGAAGCCACAGAACGATGGGAGCAGCATGCTCGCGCAGCTTACGACATATTGAG 1643
Qy 413 LysAspGlySerGlyTyrIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGly 432
Db |||||
1644 AAAGAGGTAAACCGACTTTATCTCGTGAATCTT-----GCGAAGAGATGGGA 1694
Qy 433 LeuCys---AspThrProLeuAsp-----AspMetIleLysGluIleAspLeuAsp 448
Db |||||
1695 CTAGCACCATAATGTACCAAGCCCAAGTGTCTTAGATTGGATTAGACAG----- 1742
Qy 449 AsnAspGlyLysIleAspPheSerGluPheThrAlaMetMetArgLysGlyAspGlyVal 468
Db |||||
1743 TCTGATGGTCGGGTGAGTTTACCTGGGTTTCAACCAAGCTGTACAT----- 1787
Qy 469 GlyArgSerArgThrMetMetLysAsnLeu 478
Db |||||
1788 GGAATTTCCAGCGCTGCTATCAAAAATCTC 1817
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Search completed: November 28, 2003, 15:08:29
Job time : 1208 secs